

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 144269

TO: Suryaprabha Chunduru Location: REM-2C29/2C18

Art Unit: 1637

Monday, February 14, 2005

Case Serial Number: 10/790430

From: Deirdre Arnold

Location: Biotech-Chem Library

REM 1A64

Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

Search Notes

RUSH

Please feel free to contact me if you have any questions or would like to amend the search.

Thank you for using STIC services.

Regards,

Deirdre Arnold



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### ALIGNMENTS

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APPLICANT: Notation Carl
APPLICANT: Hironaka, Catherine
APPLICANT: Hironaka, Catherine
APPLICANT: Heck, Gregory,
APPLICANT: You, Jinsong
ITILE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods
ITILE OF INVENTION: Thereof
ITILE OF INVENTION NUMBER: US/09/872,051
CURRENT APPLICATION NUMBER: 60/213,567
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR APPLICATION NUMBER: 60/240,014
PRIOR APPLICATION NUMBER: 60/240,014
PRIOR FILING DATE: 2000-10-13
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ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: source
LOCATION: (1)..(1183)
OTHER INFORMATION: 165-381 construct vector DNA
OTHER INFORMATION: 382-686 Zea maize plastid genes, rps11
OTHER INFORMATION: 687-1183 Zea maize genomic DNA
Similarity
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US-09-441-340-27/c

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; Sequence 27, Application US/09441340
; Patent NO. 6448476
; GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Phosphonate Metabolizing Pl.
FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/09/441,340
; CURRENT FILING DATE: 1999-11-16
; EARLIZER FILING DATE: 1999-11-16
; EARLIZER FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
Sequence 5, Application US/09068101
Patent No. 6372960.
GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Improved Barstar Gene
FILE REFERENCE: 2121-1399
CURRENT APPLICATION NUMBER: US/09/068,101
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: EP 96202446.9
EARLIER FILING DATE: 1996-09-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
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US-09-068-101-5/c
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US-09-441-340-27
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LENGTH: 2378
TYPE: DNA
ORGANISM: Artificial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:expression OTHER INFORMATION: cassette comprising a plant promoter linked to OTHER INFORMATION: intron, a sequence encoding an AMPA acetyl OTHER INFORMATION: transferase, and a termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: terminator
LOCATION: (2114)..(2:
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LOCATION: (1668)..(2099)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: promoter LOCATION: (28)...(965) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: transit_peptide
LOCATION: (1440)..(1667)
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US-09-970-921-5/c
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                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Frank Michiels et al.
APPLICANT: Frank Michiels et al.
TITLE OF INVENTION: Improved Barstar Gene
FILE REFERENCE: 2428-0108P
CURRENT APPLICATION NUMBER: US/09/970,921
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09970921
Patent No. 6759575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 168;
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Best Local
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LOCATION: (1999)..(3400)
OTHER INFORMATION: 1abel = PRA
OTHER INFORMATION: - contains
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LOCATION: (3677). (4003)
OTHER INFORMATION: label =
OTHER INFORMATION: end of
OTHER INFORMATION: T-DNA"
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OTHER INFORMATION: label =
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LOCATION: (4016)..(4021)
OTHER INFORMATION: label =
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LOCATION: (3399)..(3404)
OTHER INFORMATION: label =
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LOCATION: (3401)..(367)
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                                                                                   OTHER INFORMATION: Description of OTHER INFORMATION: acid, "plasmid
                                                                                                                                        ORGANISM: Artificial Sequence
                OTHER INFORMATION: label = PRAC1, "promoter region of OTHER INFORMATION: - contains an intron in the leader"
                                                   NAME/KEY: misc feature LOCATION: (1999)..(3400)
                                                                                                                                                              TYPE: DNA
 NAME/KEY:
                                                                                                                           FEATURE:
                                                                                                                                                                             ENGTH: 4032
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misc_feature
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ne synthase gene of
                                                                                      Artificial pMV71"
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                                                                                                                                     US-09-377-466B-15
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Best Local Similarity
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LCCATION: (3677).. (4003)
OTHER INFORMATION: label = 3
OTHER INFORMATION: end of n
OTHER INFORMATION: T-DNA"
NAME/KEY: misc feature
LCCATION: (3399).. (3404)
OTHER INFORMATION: label = 1
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                                                               Best Local Similarity Matches 147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REFERENCE: 38-21 (15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/09/377,466B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
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LOCATION: (4016)..(4021)
OTHER INFORMATION: label =
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OTHER INFORMATION: label
                                                                                                                                                       LOCATION: (1490)..(3448)
OTHER INFORMATION: Cry3Bb1 variant v11231
NAME/KEY: terminator
LOCATION: (3475)..(3730)
OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription
OTHER INFORMATION: termination and polyadenylation sequence
                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description OTHER INFORMATION: cassette
                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                      NAME/KEY: intron
LOCATION: (669)..
                                                                                                                                                                                                                                                                                                                                          NAME/KEY: promoter
LOCATION: (25)..(640)
OTHER INFORMATION: P-CaMV.35S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                  NAME/KEY: CDS
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                        GACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGC
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                                                                                12.4%; Score 147; DB 4; 100.0%; Pred. No. 3e-62;
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nopaline
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Pred. No.
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RESULT 7
US-09-186-002-16
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US-09-377-466B-13
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Best Local
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NAME/KEY: transit peptide
LOCATION: (1489)..(1635)
OTHER INFORMATION: amino terminal TS
NAME/KEY: intron
LOCATION: (1636)..(1798)
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb
FILE REFERENCE: 38-21 (15304) Cry3Bb Improved Exp.
CURRENT APPLICATION NUMBER: US/09/377,466B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: terminator
LOCATION: (3871)..(4127)
OTHER INFORMATION: T-AGREU.nos 3' transcription termination
OTHER INFORMATION: polyadenylation sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (1885)..(3843)
OTHER INFORMATION: Cry3Bb1 variant v11231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: transit_peptide
LOCATION: (1799)..(1885)
OTHER INFORMATION: carboxy terminus TS-Zm.rbcS
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LOCATION: (25)..(640)
OTHER INFORMATION: P-CaMV.358
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OTHER INFORMATION: I-Zm.rbcS
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LOCATION: (669)..(1472)
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                                                                                                                                                                                                                                                                                           al Similarity
147; Conserv
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                                                                                     GTTACTAGATCGGGGATATCCCCGGGG 4142
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                             12.4%; Score 147; DB 4;
100.0%; Pred. No. 3e-62;
tive 0; Mismatches
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                                             Matches 147;
                                                             Query Match
Best Local
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                                                                                                                                                                                         ORGANISM: Artificial SequesarTURE:
NAME/KEY: unsure
LOCATION: (3597)...(3670)
OTHER INFORMATION: "n" = 9
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                                                                                                                                                                                                                                                                                                                                       APPLICANT: Corbin, David R.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Method for Transforming Plants to
TITLE OF INVENTION: delta-Endotoxins
FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
CURRENT FILING DATE: 1998-11-04
NUMBER: US/09/186,002B
CURRENT FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
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LOCATION: (3666)...
OTHER INFORMATION:
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TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                          NAME/KEY: unsure
LOCATION: (4292)..(4344)
OTHER INFORMATION: "n" =
                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                           Local
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Pred. No. 2.9e-62;
0; Mismatches 0;
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; NAME/KEY: unsure
; LOCATION: (4355)..(4407)
; OTHER INFORMATION: "n"
US-09-186-002-15
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US-09-186-002-15
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US-09-186-002-13
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APPLICANT: Corbin, David R.
APPLICANT: Romano, Charles P.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Method for Transforming Plants to
TITLE OF INVENTION: delta-Endotoxins
FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
CURRENT APPLICATION NUMBER: US/09/186,002B
CURRENT APPLICATION NUMBER: US/09/186,002B
CURRENT FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
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Patent No. 6489542
                                             APPLICANT: Corbin, David R.
APPLICANT: Romano, Charles p.
TITLE OF INVENTION: Improved Method for Transforming Plants to
TITLE OF INVENTION: Improved Method for Transforming Plants to
TITLE OF INVENTION: delta-Endotoxins
TILE REFERENCE: 38-21(13547) US pat No. 6489542 09/186,002
CURRENT APPLICATION NUMBER: US/09/186,002B
CURRENT FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
                                                                                                                                                                                                                   Sequence 13, Application US/09186002B Patent No. 6489542 GENERAL INFORMATION:
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Best Local Similarity
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TYPE: DNA
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NAME/KEY: unsure
LOCATION: (3660)..(3773)
OTHER INFORMATION: "n" =
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ORGANISM: Artificial Sequence
                              LENGTH: 10339
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1 GACGTTATTTATGAGATGGGTTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGC

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Sequence 27, Application US/09441340

Patent No. 643476.

GENERAL INFORMATION:

APPLICANT: Barry, Gerard F.

TITLE OF INVENTION: Phosphonate Metabolizing Plants
FILE REFERENCE: 38-21(15303)

CURRENT APPLICATION NUMBER: US/09/441,340

CURRENT FILING DATE: 1999-11-16

EARLIER APPLICATION NUMBER: 60/108,763

EARLIER APPLICATION NUMBER: 60/108,763

EARLIER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 27

SEQ ID NO 27
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, NAME/KEY: unsure
; LOCATION: (4382)...(4434)
; OTHER INFORMATION: "n" =
US-09-186-002-13
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                                                             ; LOCATION: (2114)..(2369)
US-09-441-340-27
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 Query Match
Best Local S
Matches 140
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Best Local Similarity
Matches 147; Conserv
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LOCATION: (3687)...
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2378
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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LOCATION:
                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence:expression OTHER INFORMATION: cassette comprising a plant promoter linked to OTHER INFORMATION: intron, a sequence encoding an AMPA acetyl OTHER INFORMATION: transfer
                                                                                NAME/KEY: terminator LOCATION: (2114)..(2)
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(966)..(1423)
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11.8%; Score 140; DB 3; llarity 100.0%; Pred. No. 8.5e-59; Conservative 0; Mismatches 0;
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Pred. No. 2.9e-62;
0; Mismatches 0;
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US-09-441-340-31
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Sequence 23, Application US/09441340 Patent No. 6448476
                                                                                                                                                                                                                                                                                        Query Match 11.8%;
Best Local Similarity 100.0%;
Matches 140; Conservative
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LENGTH: 2436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/441,340
CURRENT FILING DATE: 1999-11-16
EARLIER APPLICATION NUMBER: 60/108,763
EARLIER FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
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OTHER INFORMATION: 5
OTHER INFORMATION: 6
OTHER INFORMATION: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: terminator LOCATION: (2172)..(2:
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LOCATION: (670)..(1473)
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LOCATION: (1726)..(2157)
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APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Phosphonate Metabolizing Pl.
FILE REFERENCE: 38-21(15303)
CURRENT APPLICATION NUMBER: US/09/441,340
CURRENT FILING DATE: 1999-11-16
EARLIER APPLICATION NUMBER: 60/108,763
EARLIER FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 23
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Best Local S
Matches 137
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APPLICANT: Barry, Gerard

APPLICANT: Cheikh, No. 6441277dine

APPLICANT: Kishore, Ganesh

TITLE OF INVENTION: Expression of I

TITLE OF INVENTION: Aldolase in Tra
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NAME/KEY:
LOCATION:
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
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APPLICANT: Barry, Gerard

APPLICANT: Cheikh, No. 6663906dine

APPLICANT: L1899.0186.DVUS02 (MOBT:086-2)

FILE REFERENCE: 11899.0186.DVUS02 (MOBT:086-2)

CURRENT APPLICATION NUMBER: US/10/164,204

CURRENT PILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: 09/098,219

PRIOR APPLICATION NUMBER: 09/098,219

PRIOR FILING DATE: 1998-06-16

NUMBER OF SEQ ID NOS: 6
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Best Local Similarity 100.0%; Pred. No. 2.4e-57;
Matches 137; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                      SOPTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 10846
                                                                                                                               Query Match 11.6%; Score 137; DB 4; Length 10846; Best Local Similarity 100.0%; Pred. No. 2.4e-57; Matches 137; Conservative 0; Mismatches 0; Indels 0
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PRIOR APPLICATION NUMBER: US 60/049,995
APPLICATION NUMBER: US 60/049,995
FILING DATE: 17-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 713-787-1440
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10846 base pairs
                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: P-FMV/CTP1/fda/NOS3'
                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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TYPE: nucleic acid
STRANDEDNESS: double
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BI650935
BU702841
BG076391
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5630.828 Million cell updates/sec
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Compugen Ltd.
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AA103332 mo24d04
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CF916734 B0999F07-
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ih42b06.x

603297263

UI-M-FC0-
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                          H3159C09-
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AUTHORS
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
                                                                                                                                                         MGI:1435432
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ALIGNMENTS

Other ESTS: uz73a01.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml BF450993 BF450993.1 GI:11517162 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 354) Seq primer: -40RP from Gibco High quality sequence stop: 340. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Mus musculus (house mouse) /tissue type="spontaneous
Stem cell origin."
/lab_host="PH10B" organism="Mus musculus" /mol_type="mRNA" /strain="CZECH II" /db_xref="taxon:10090" /clone="IMAGE:3674664" Location/Qualifiers musculus mRNA linear EST 29-DEC-200 lus cDNA clone IMAGE:3674664 5', tumor, metastatic EST 29-DEC-2000 ő mammary. ц

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TITLE
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AA103332
AA103332.1 GI:1649616
EST.
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517 bp mRNA linear EST 12-MAR-2002 ih42b06.yl Melton Mouse E16 5 Pancreas Library 2 M16B2 Mus musculus CDNA clone IMAGE:5679706 5', mRNA sequence.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubgesel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGCTGTTCTGCTGACTTT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:335295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -28M13 rev1 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                             100.0%; Score 18; Diclarity 100.0%; Pred. No. 13
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                       /clome lib="Life Tech mouse embryo 13 5dpc 10666014"
/note="Organ: whole embryo; Vector: pCMY-SPORT2; Site
SalI; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dT. 13.5dpc embryos. pCMV-SPORT2 vector."
                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="embryo"
/dev_stage="13.5dpc embryos"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="IMAGE:554503"
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylle, T., Martin, J., Blistain, A., Schmitt, A., Thelsing, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
                                                                                                                                                                              BE626708 S18 bp mRNA linear EST 24-AUC unl0e66.y2 Soares mammary gland NMLMG Mus musculus cDNA clone IMAGE:3371554 5' similar to SW: KRUH DROME P08155 KRUEPPEL
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu)
MGI:1957584 This sequence now available from the IMAGE consortium, for clone orders contact: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endocrine Pancreas Consortium 
Unpublished (2000)
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EST.
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Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Douglas Melton, Klaus H. Kaestner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                           Mus musculus
                                                                                                               BE626708.1
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                                                                                                                                                           HOMOLOGOUS PROTEIN ;, mRNA sequence.
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Washington University Genome Sequencing Center For information o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: dmelton@biohp.harvard.edu
                                                                 Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="ICR"
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/clone="IMAGE:5679706"
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/lab_host="TOP10"
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TITLE
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B0999F07-5 NIA Mouse Unfertllized Egg cDNA Library
musculus cDNA clone NIA:B0999F07 IMAGE:30481794 5',
CF916734
CF916734.1 GI:38187936
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases ב נט שבט, NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                               Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: 80999 row: F column: 07
Seq primer: M13 Reverse
High quality sequence stop: 522
                                                                                                                                                                                                                                                                                                                           Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplif
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 522)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                            Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                     21429098
                                                                                                                                                                                                                                                                                        Genome Res. 11 (9), 1553-1558 (2001)
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                                                                             quality sequence stop: 522
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/mol type="maNA"
/db_xref="taxon:10090"
/clone="IMAGE:3371554"
/sex="female (lactating)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="Soares mammary_gland_NMLMG"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
                                    Location/Qualifiers
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/organism="Mus musculus"
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Query Match
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529 bp mRNA linear EST 19-NOV-2002 K0222G09-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus musculus cDNA clone NIA:K0222G09 IMAGE:30046832 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                   Other ESTs: K0222G09-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
                                                                                                                                                                                                                                                                                          Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Stagg,C., Martin,P., Aiba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                     Unpublished (2001)
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1 (bases 1 to 529)
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Mammalia; Eutheria; Rodentia;
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                                                                            Seq primer: M13 Reverse
                                                                                                    Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0222 row: G column: 09
                                                                                                                                            National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
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                                                        quality sequence stop: 529
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/strain="C57BL/6J"
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/dev_stage="Unfertilized Egg"
/lab_host="DH10B"
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/db_xref="taxon:10090"
Location/Qualifiers
1. .529
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                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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strain="C57BL/6J"

_type="mRNA"

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1MAGE:3371554 3', mRNA sequence.
BE632036
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                                                                                                                                                                       Unpublished (1997)
Other ESTs: uul0e06.y2
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                       MGI:1081158
                                                                                                                                                                                                                                                                                                                                       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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1 (bases 1 to 534)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                       quality sequence stop: 469.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo (dT) primer [Invitrogen:
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/mol_type="mRNA"
/db_xref="taxon:10090"
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/db_xref="taxon:10090"
/clone="NIA:K0222G09_MAGE:30046832"
                  /organism="Mus musculus"
/mol_type="mRNA"
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/lab_host="DH10B"
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Endocrine Pancreas Consortium Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                               Fax: 617-495-055, Email; dmelton@biohp.harvard.edu
Email; dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by
Washington University Genome Sequencing Center For information
Washington University Genome Sequencing Center For information
Washington University Genome Sequencing Center For information
                                                                                                                                                                                                                                                                                                   obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu)
MGI:1953252 This sequence now available from the for clone orders contact: info@image.llnl.gov
High quality sequence stop: 449.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MA 02138
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 540)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           617-495-1812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                     /sex="Both for embryonic & newborn, male for adult and adult islet"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares_mammary_gland_NMLMG"
/note="Vector: pT7T3D-Pac (Pharmacia) with
polylinker; 1st strand cDNA was prepared fi
                                         /dev_stage="Embryonic day
adult, mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="mammary gland"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:5666926"
                                                                                                                                                                                                           organism="Mus musculus"
mol_type="mRNA"
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clone_lib="Melton Normalized Mixed Mouse
                      lab_host="DH10B"
                                                                                                                                                                                       strain="ICR"
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BU605257
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VERSION
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Matches
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                                                                                                                                                                                                                                 source
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mah89b07.yl McCarrey Eddy 18 day leptotene and zygotene
spermatocytes Mus musculus cDNA clone IMAGE:6367453 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                    Library constructed and donated by J. McCarrey, Ph.D. (Southwest Foundation for Biomedical Research, Dept. of Genetics) - excision done by E.M. Eddy, Ph.D. (National Institutes of Health, National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIEHS Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McCarrey,J., Eddy,M., Marra,M., Hillier,L., Clifton,S., Pape,D. Martin,J., Wylie,T., Dante,M., Bowers,Y., Theising,B., Gibbons,I Ritter,E., Tsagareishvili,R., Ronko,I., Maguire,L., Kennedy,S., Bennett,J., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                       MGI:2044885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIEHS Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: McCarrey/Eddy NIEHS Mouse
                                                                                                                                                                                                                                                                                                                                                               Institute of Environmental Health Sciences).
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                                                                                                                                                                                                                                                      quality sequence stop: 421.
Location/Qualifiers
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314 286 1810
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spermatocytes"
                        /tissue type="18-day leptotene and zygotene spermatocytes"
/lab_host="DH108 (phage-resistant)"
/clone_lib="McCarrey Eddy 18 day leptotene and zygotene
                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6367453"
                                                                                                     sex="male"
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CF171411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TGCTGTTCTGCTGACTTT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H. Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0842 row: B column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21429098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 11 (9), 1553-1558 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: M13 Reverse
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(Stratagene); Site_1: EcoRI; Site_2: XhoII; cDNA oligo
dT-primed [5'-(cA)I0-ACTAGTCTCGAGTTTTTTTTTTT-3'] and
directionally cloned using 5' linkers 5'-AATCGGCACGAG-3'
and 5'-CTCGTGCCG-3'. Size selection of >400bp material
gives average insert size ranging from 1-2 kb. Library was
mass excised (from lambda-UniZAP-XR) and resulting
singl-stranded phagemids were prepped and tranformed into
DH10B. Library constructed and donated by J. McCarrey,
Ph.D. (Southwest Foundation for Biomedical Research, Dept.
of Genetics); excision done by E.M. Eddy, Ph.D. (National
Institutes of Health, National Institute of Environmental
Health Sciences)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop: 557
/organism="Mus musculus"
/mol type="mRNA"
/mol type="mRNA"
/strain="C57BL/6J"
/strain="C57BL/6J"
/db_xref="niaEST:B0842B01-5"
/db_xref="taxon:10090"
                                                                                                                                                                                                                 /dev_stage="Newborn Kidney"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                          /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
                                                                                                                                                                                                                                                          clone="NIA:B0842B01 IMAGE:30471468"
                                                                                                                                                                                      lone_lib="NIA Mouse Newborn Kidney cDNA Library (Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 18; 100.0%; Pred. No.
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KEYWORDS

FEATURES

treated with T4 DNA polymerase, and

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DEFINITION
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Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    576 bp mRNA linear EST 31-At L0303E07-3 NIA Mouse Newborn Ovary cDNA Library Mus musculus clone L0303E07 3', mRNA sequence.
AW559055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 576)
Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, W.H. III, Becker, K.G. and Ko, M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW559055
AW559055.1 GI:7204484
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLYA=Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: George J. Kargul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10922068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCTGTTCTGCTGACTTT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH103 E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.0 kb. The library was constructed by Yulan Piao."
                                         /mol_type="mRNA"
/strain="C57BL/60"
/db_xref="niaEST.L0303E07-3"
/db_xref="taxon:10090"
                                                                                                                                                                                                   dev_stage="Newborn Ovary"/lab_host="DH10B"
                                                                                                                                                                                                                                                 'sex≃"female"
                                                                                                                                                                                                                                                                        clone="L0303E07"
                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
    of to
total RNA . The double-stranded cDNAs were th T4 DNA polymerase and purified by
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Pred. No. 13;
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REFERENCE

AUTHORS

SOURCE KEYWORDS

VERSION ACCESSION 밁 á

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Best Loc Matches

RESULT 11

ORIGIN

FEATURES

FEATURES

COMMENT

COMMENT

MEDIINE JOURNAL TITLE

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DEFINITION
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BM219770/c
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MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C0929G10-3 NIA Mouse 12.5-dpc
Library (Long) Mus musculus cD
3', mRNA sequence.
BM219770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Dec 14, 2001 this sequence version replaced gi:17779692. Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -21M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0929 row: G column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11544199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21429098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 11 (9), 1553-1558 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM219770.2 GI:31478468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
1 (bases 1 to 598)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCTGTTCTGCTGACTTT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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/clone_lib="NIA Mouse 12.5-dpc Male Genital Ridge/Mesonephros cDNA Library (Long)" /note="Vector: pSPORT1 (Invitrogen); Site_1: Sall; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
                                                                                                                                                             /tissue_type="Male genital ridge/mesonephros"
/dev_stage="12.5-dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ethanol-precipitation. The cDNAs were ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                     clone="NIA:C0929G10 IMAGE:30037425"
                                                                                                                                                                                                                                                                                             db_xref="niaEST:C0929G10-3"
db_xref="taxon:10090"
                                                                                                                                                                                                                                            sex="Male"
                                                                                                                                                                                                                                                                                                                                                 'strain="C57BL/6J"
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 bp mRNA linear EST 07-JUN-200
5-dpc Male Genital Ridge/Mesonephros cDNA
lus cDNA clone NIA:C0929G10 IMAGE:30037425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 07-JUN-2003
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REFERENCE

AUTHORS TITLE

SOURCE VERSION ACCESSION KEYWORDS

a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 

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REFERENCE
AUTHORS
TITLE
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CF739008
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KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF739008 603 bp mRNA linear UI-M-HDO-cku-p-16-0-UI.rl NIH_BMAP_HDO Mus musculus IMAGE:30610839 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 603)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CF739008
CF739008.1 GI:37635345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: pYX-5
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/clone="IMAGE:30610839"
/tissue_type="whole eye"
/tissue_type="whole eye"
/dev_stage="embryo 12.5,13.5,14.5 dpc"
/dev_stage="embryo 12.5,13.5,14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NNH_BMAP_HD0"
/note="Organ: Eye; Vēctor: pXX- Asc; Site_1: EcoR I;
/note="Organ: Eye; Vēctor: pXX- Asc; Site_1: EcoR I;
/site_2: Not I; The library was constructed according
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site_Double strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ion/Qualifiers
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CF916509
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B0996C03-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus
musculus cDNA clone NIA:B0996C03 IMAGE:30481466 5', mRNA sequence.
CF916509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H. Construction of long-transcript enriched
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0996 row: C column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 605
size selected according to mRNA size fraction ,ligated with EcoR I adaptor , digested with NotI and then cloned directionally into pYX-Asc vector . The library tag sequence located between the Not I site and the polyA tail is TTATTGAACT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                /db_xref="niaEST:B0996C03-5"
/db_xref="taxon:10090"
/clone="NIA:B0996C03_IMAGE:30481466"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                            /dev_stage="Unfertilized Egg"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                               strain="C57BL/6J"
                                                                                                                                                                                                                                                                                       clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 18;
100.0%; Pred. No.
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Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA-libraries from spiningrogram amounts of total RNAs by a universal PCR amplification
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Seq primer: -21M13 Forward
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BM237875.2 GI:31494430
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Plate: K0508 row: E column: 08
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/clone_lib="NIA Mouse Hematopoietic Stem Cell (Lin-/G-Kit+/Sca-1+) cDNA Library (Long)" (Long)" (Mouse collaboration of Genetics, Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
                                                                                                                                                                                                                                     /tissue_type="Hematopoietic Stem Cell (Lin-/c-Kit+/Sca-1+)" (dev stage="Age approx.10 weeks old" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6NCr"
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/clone="NIA:K0508E08 IMAGE:30064663"
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Query Match Best Local ( 100.0%; Score 18; DB Pred. No. 13; 4. Length 609;

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Matches 18 Similarity Conservative <u>.</u> Mismatches 0 Indels <u>.</u> Gaps 0

밁 S 504 TGCTGTTCTGCTGACTTT 487 ۳ TGCTGTTCTGCTGACTTT 18

Search completed: Job time : 124.68 Becs February 10, 2005, 17:01:59

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7855.666 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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            AX342368 Sequence
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## ALIGNMENTS

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Qy 1	Qy 1 Db 1	₽	Qy	Db	δλ	Query Match Best Local Matches 49	ORIGIN				source	FEATURES	JOURNAL	TITLE	AUTHORS	REFERENCE	OKOM TON	CECANTEN	KEYWORDS	VERSION	DEFINITION	AX342368	RESULT 1
181 AGCCGCCGTCGCCATTCGGCCAGACTCCTCCTCTCTCGGCATGAGCCGATCTTTTCTCTG 240	121 GAGGTAAACAGATCAGCATCAGCGCTCGAAAGTTTCCTCAAAGGATGCGGAACTGTTTCC 180		61 TCCAGGGTGAAGTATCAGAGGATTTACCGCCCATGCCTTTTATGGAGACAAGAAGGGGAG 120	1 AATCGATCCAAAATCGCGACTGAAATGGTGGAAGAAGAAGAGAGAG	1 AATCGATCCAAAATCGCGACTGAAATGGTGGAAGAAGAGAGAG	/ Match 100.0%; Score 498; DB 6; Length 498; Local Similarity 100.0%; Pred. No. 8.2e-264; nes 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		/note="1-304 Zea maize genomic DNA 305-349 construct vector DNA 350-498 rice actin 1 promoter DNA"	/mol_type="unassigned DNA" /db xref="taxon:32630"	/organism="synthetic construct"	1498	MonBanto recumorogy are (03) Location/Qualifiers	EP 1167531-A 7 0	for detection thereof			other sequences: artificial sequences.	aynthetic construct	and the state of t	AX342368.1 GI:18151811	7 from Patent EP1167531.	AV142769 498 bp DNA linear PAT 12-JAN-2002	

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Unclassified.
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Patent: EP 1167531-A 8 02-JAN-2002;
Monsanto Technology LLC (US)
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                                                                               27
                                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
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/db xref="taxon:32630"
/db xref="taxon:32630"
/note="1-164 Agrobacterium tumefaciens nos 3' terminator
/note="1-164 Agrobacterium tumefaciens nos 3' terminator
165-81 construct vector DNA 382-686 Zea maize plastid
genes, rps11 and rpoA 687-1183 Zea maize genomic DNA"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
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S44221
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                                                                                                                                                                                                                                                                                                                                                                                                                   transformation 
Plant Cell 2 (2), 163-171 (1990)
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                                         TACTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGG
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(bases 1 to 1266)
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Conservative (
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1246. .1266
/gene="Act1"
/note="actin 1"
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/protein_id="AAD13837.1"
/db_xref="GI:4261543"
                                                                                                                                                                                                                                                                                      organism="Oryza sativa"
/mol_type="genomic DNA"
/db_xref="taxon:4530"
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                                                                                                                                                                                                                                                              gene="Act1"
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Unknown.
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Sequence 7 from patent
ISO115
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Oryza sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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McElroy, D. and Wu, R.
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                                                                                                                                                                                        ZENECA LIMITED (GB)
Location/Qualifiers
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Patent: WO 0066748-A 49 09-NOV-2000;
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Similarity 100.0%; F
70; Conservative 0;
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/mol_type="unassigned DNA"
                                                                                                                                          /organism="Oryza sp."
/mol_type="unassigned DNA"
/db_xref="taxon:52841"
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Oryza sp.
Oryza sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Vagnoliophyta; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                    Sequence 5 from patent US 5641876.
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Sequence 44 from Patent
AX044144
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Patent: WO 0066747-A 44 09-NOV-2000;
ZENECA LIMITED (GB)
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McSlroy,D. and Wu,R.

Rice actin gene and promoter

Patent: US 5641876-A 5 24-JUN-1997;

Location/Qualifiers
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Unclassified.
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                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reporter vector pActXYN, AY452735
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Lucia, QLD 4072, Australia
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/note="from rbcS gene"
4895
/note="SP6 RNA polymerase transcription initiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="sXynA"
3800. .4513
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3339. .3792
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/protein_id="AAR29085.1"
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McElroy, D. and Wu, R
Rice actin gene and
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                                                                                                                                   note="unnamed protein product; Beta-lactamase
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patent US 5641876.
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/note="Ubi-promoter from maize"
/note="Ubi-promoter from maize"
/921. .6400
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6401. .6672
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/note="Poly-A signal
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9120. .9359
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                                                                                                                                                                                                                                                                                                  /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

El (bases 1 to 147344)

El (bases 1 to 147344)

Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M.,

Overton II, L.L., Tsitrin, T., Kim, M.M., Bera, J.J., Jin, S.S.,

Fadrosh, D.W., Tallon, L.J., Koo, H., Zismann, V., Hsiao, J., Blunt, S.,

Vanny, Q.O., Haas, B.J., Suh, B.B., Peterson, J.J., Quackenbush, J.,

White, O., Salzberg, S.L. and Fraser, C.M.

Oyyza sativa chromosome 3 BAC OSJNBa0078A17 genomic sequence
                                                                                                                                                                                                                                         Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan and Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://GCR-081.mit.edu/GENSCAN.html), GeneMark/), and GeneSplicer (Mihaela Perrea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without proteins are named as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://comms.wistla.div/sahu/cpnharan-ce/) cimple remarks are
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Oryza sativa chromosome 3 BAC OSJNBa0078A17 genomic sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-NOV-2002) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA (bases 1 to 147344)
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The orientation of the sequence is from SP6 to T7 end of
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                                                                                                                                                               http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                              \begin{array}{ll} \text{http://genome.wustl.edu/eddy/trNAscan-SE/). Simple repeats are} \\ \text{identified by repeatmasker (Arian Smit,} \end{array} 
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                                                                                                                BAC overlaps with rice BACOSJNBa0014G15
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organism="Oryza sativa/mol_type="genomic DNA"
                                                                                  'ocation/Qualifiers
                                (japonica cultivar-group)"
                                                                                                                      (AC090882)
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/gene="OSJVBA007BA17.2"
complement(join(8447. .8572,8747. .8812,10002. .10187, 10261. .10798,10947. .11020))
/gene="OSJVBA0078A17.2"
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complement (8447. .1120)

/gene="OSJNBa0078A17.2"

/note="predicted by fgenesh"

complement (join(<8447. .8572,8747. .8812,10002. .10187,
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CFCVSTSTYAASVEALAALPVDYLRSRHFRVVTIYRERLSKRE-LVTVREELRCLLDWK
HLEPPLOLPFWYTCTERLOFMLFKFSVWKRHROOD-CQREEDVIDLLOCKRKKKELLDAK
EVVVDRLLEHGSGAEMTRQAVRDAARGAIGDTGLLDFVIKSLGDTIVGNYIVRRVPDA
ETRVLHESLEEYEEPTPALLDVEVECTFLFPVVRWSTWSTUSCHAVYRAWDEVRSS
AAQAVLDCKHWYKWWGLGDESDDDLRFFVEWGPOPWEBAFELIRPMFLGEIVVVPLHS
AAQAVLDCKHOLDSSHODLRFFVEWGOPWEBAFELIRPMFLGEIVVVPLHS
MGELLVESEHALRDTYYFFEEFQAEGLHGIAGEKWDPVNLGGAENGDTISVYGNGADM
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TTSSSSSSASAAPAAGAPRVYELRDPPGREAGLGGAFRANUWWILLRQMGGASPAS
PAAGGPGSASAAVAVAMVULLSDDRTGVVVELFAVEERVASSPKPLCDYCRWAGWSHH
WVSKRKYHFIIPAPADWDRQLAADVILGRTDHLLHGLIHSNGFGHLVMLRGRDGGSTA
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complement(join(<890. .2270,2551. .2797,3430. .>3895))
/gene="OSJNBa0078A17.1"
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VLCGGALMAAGPINS"
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/gene="OSJNBa0078A17.1"
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complement(890. .3895)
                     /rpt
18206
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                                                                                                                                                                                                                                                                                                                                                                                                            VKDAAVPGETSSISTLFAKKNVGAVLMDKEAPWKASPVAIESQYSRTGDPDCF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein"
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/brotein id="AA038820.1"
/db xref="G1:28301927"
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/clone="OSJNBa0078A17"
rpt_family="tandem"
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1392 bp
Sequence 6 from patent US 5641876.
ISO114
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(gene="0SJNBa0078A17.4"
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25833. .25973
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ASLATAPLQALMINNQ GENQFIGS I SP I SNNTSLGEIMLHSNDFTGPLDPSGLASL
SDLEILRDNQTGPVPDSLLKLGSLTKVTLTNNLLQGPTPKFADKVKADVVPTTERFCLL
STPGQPCDFRVNLLLEVAAEFQYPAKLADNWKGNDFCDGYIGVGCDAGNITVLNFARM
GFSGS I SPAIGKITTLCKLI LADNNITGTVPKEVAALPALTEVDLSNNNLYGKLPTPA
AKNULVKANGNPIGKDAPAPSGSGSGSGSNAPDGSNGSNGSSSSSSASGII AGSV
VGAIAGVGLLAALGFYCYKRKQKPFGRVQSPHAMVVHPRHSGSDPMVKITVAGGNVN
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ELHDGTKIAVKRMEAGVMGNKGLNEFKSEIAVLTKVRHRNLVSLLGYCLDGNERILVY
EYMPQGTLSQHLFEWKEHNLRPLEWKKKLSIALDVARGVEYLHSLAQQTFIHRDLKPS
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/note="predicted by fgenesh"
complement(<20076. >20474)
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LTALARLELFDNSISGELPSLAGLSSLQYLLVHNNGFTRIPPDFFKGLTALAAVSLDN
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/gene="OSJNBa0078A17.4"
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22377. .22404
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gsgggrhwigdgglgnrilaaasaflyavltarvllvdtsnemdelfsepppgtawll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
/protein_id="AAO38822.1"
/db_xref="GI:28301929"
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                                                                                                                                                                                                                                                                                                                                                                14.1%; Score 70; DB 8; Length 147344; 100.0%; Pred. No. 7.4e-27;
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McElroy,D. and Wu,R.
Rice actin gene and promoter
Patent: US 5641876-A 6 24-JUN-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z29587.1 GI:452344 ampicillin resistance; beta-lactamase; colel origin; expression vector; nos terminator; phage fl region; rice actin1 promoter.
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                                                                                                                                                         Direct Submission
Submitted (26-JAN-1994) Liu L.,
Research, Colney Lane, Norwich,
Location/Qualifiers
                                                                                                                                                                                                                                                                       Liu,L., Dasgupta,I., Davies,J.W. and Hull,R. Modified vectors for monocot transformation toward virus resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other sequences; artificial sequences.
1 (bases 27 to 282)
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             /note="start codon for 27. .282
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                                                                                                      organism="synthetic construct"

ol_type="other DNA"
/note="nos terminator'
                                                            note="multiple cloning sites"
                                                                                            xref="taxon:32630"
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                              gene expression"
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506. .962
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3181. .4412
/note="rice actin 1 5'
/citation=[2]
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IELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDAGGEQLGRRIHYMGDHVTRL
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
DRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQOLIDWMEADKVAGPL
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Copyright (c) 1993 - 2005 Compugen Ltd.
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ω	16		559	8	AY296477
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ALIGNMENTS

#### 1183 bp Sequence 8 from Patent EP1167531. AX342369 AX342369.1 GI:18151812 Behr, C.F., Hironaka, C., Heck, G.R. and You, J. Corn transformant pv-zmgt32 (nk603) and compositions and for detection thereof Patent: Ep 1167531-A 11 02-JAN-2002; Monsanto Technology LLC (US) Location/Qualifiers synthetic construct synthetic construct other sequences; artificial sequences. Sequence 11 from Patent AX342372 synthetic construct synthetic construct AX342372.1 AX342372 Similarity 100. 18; Conservative TGCTGTTCTGCTGACTTT 18 TGCTGTTCTGCTGACTTT 18 organism="synthetic construct" mol_type="unassigned DNA" db_xref="taxon:32630" /note="Zea maize genomic DNA and vector DNA" GI:18151815 100.0%; 0; Score 18; DB 6; Length 18; Pred. No. 5.8; 18 bp : EP1167531. Mismatches DNA 0; Indels linear PAT 12-JAN-2002 PAT 12-JAN-2002 0 Gaps methods 0

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                                                                                                                                                                                                                                                                                                                                                                                     Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generath, A., Schein, J.E., Jones, S.J., and Marra, M.A.
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                                                                                                                                         Submitted (01-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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Corn transforment pv_zmgt32 (nk603) and compositions and methods
                                                                                                                                                                                                                       Director MGC Project.
Direct Submission
                                                                                                                                                                                                                                                                                                                                            Generation and initial analysis of more than 15,000 human and mouse cDNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus zinc finger protein 445, mRNA (cDNA clone IMAGE:6410700), complete cds.
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/mol_type="unassigned DNA"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausmer, R.D., Collins, F.S., Wagner, L., Sheamen, C.M., Schuler, G.D. Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Mus musculus zinc finger protein 445, IMAGE:4018895), partial cds.

2699

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mRNA mRNA

(cDNA clone

ROD 12-OCT-2004

BC034572.1 GI:21961272

Mus musculus (house mouse)

BC034572

BC034572

Eukaryota; Mus musculus

; Metazoa; Chordata; Eutheria; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

Mus.

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(bases 1 to 2699)

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Query Match
Best Local
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1868
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This clone has the following problem: The cds is short compared the longest cds in the locus.
Location/Qualifiers
                                               1 TGCTGTTCTGCTGACTTT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford Universiting Group at the Stanford, Stanford, Center, Stanford Universiting Group of Medicine, Stanford, Web site:

Meb site:

Meb site:

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                         Similarity
TGCTGTTCTGCTGACTTT 1885
                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE: 6410700"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . .2386
                                                                                                                       100.0%; Score 18; DB 10; 100.0%; Pred. No. 4.4;
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lib="NIH_BMAP_FOO"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 41 Row: d Column: 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Director MGC Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12477932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue type="Mammary tumor metastatized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." (clone lib="NCI CGAP_Lu29"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                         codon_start=2
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FEATURES

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20892-2590

REMARK COMMENT

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Gaps

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н., JOURNAL PUBMED REFERENCE AUTHORS SOURCE ORGANISM RESULT 5 BC027167 ACCESSION VERSION 밁 Ś REFERENCE COMMENT KEYWORDS DEFINITION Pocus Query Match Best Local : AUTHORS REMARK JOURNAL TITLE Strausberg, R.D., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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Generation and initial analysis of more than 15,000 full-length 2181 TGCTGTTCTGCTGACTTT 2198 18; 1 TGCTGTTCTGCTGACTTT 18 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center BC027167.1 Direct Submission
Submitted (04-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer Mus musculus z835 bp mRNA linear ROI Mus musculus zinc finger protein 445, mRNA (cDNA clone IMAGE:4953934), partial cds. BCO27167 NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Eukaryota; Kowis, C.R., Sneed, A.J., Martin, R.G., A.N., Gibbs, R.A. Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu Director MGC Project. human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. Similarity Center code: BCM-HGSC Institute, 31 Center Drive, Room 11A03, (bases 1 to 2835) (bases 1 to 2835) Conservative Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Nutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus GI:20071802 (house mouse) 100.0%; 0 Score 18; Pred. No. Mismatches 99 (26), DB 10; 0 16899-16903 (2002) Bethesda, Length 2699; ž

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AUTHORS
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AY341877
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Zhou,G., Wany, Direct Submission
Direct Submission
Submitted (14-JUL-2003) Dept. of
No 220, HanDan Rd., Shanghai, S
No 220, Location/Qualifiers
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Location/Qualifiers
                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 3788).
                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                 Zhou, G., Wang, J. and Zhang, Y. Cloning of mouse zinc finger protein 445
                                                                                                                                                                                                                                                                                                                                                          AY341877.1 GI:33638102
                                                                                                                                                                                                                                                                                                                                                                             Mus musculus zinc finger protein AY341877
                                                                                                                                                                                                                                                                                                                                                                                                                       AY341877
                                                                                                                                                           Unpublished
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                                                                                                                                          (bases 1 to 3788)
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/db_xref="LocusID:235682"
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/mol_type="mRNA"
/strain="FVB/N"
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Pred. No. 4.3;
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                                                of Genètics, Institute of Genetics,
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Submitted (24-JUN-2002) Genome Sequencing
or rowin MO 63108, USA
                Submitted (03-APR-2003) Genome Sequencing Center, Parkway, St. Louis, MO 63108, USA 5 (Dases 1 to 175440) McPherson, J.D. and Waterston, R.H.
                                                                                                   Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 175440) McPherson, J. D. and Waterston, R.H. Direct Submission
                                                                                                                                                                                                                                                                                                                          Dignan,G. and Haglund,K.
The sequence of Mus musculus
Unpublished (2001)
2. (bases 1 to 175440)
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 175440)
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    Direct Submission
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GLKESFKQKSRLQTSCGDSIQMKEMKEGADISQRTGRESEVLANNDILELKHVKCVSV
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SKKRLSFKHGYDRNFRKSSHYNNKYGEGLRGTGEGFGVYQNTGLKENGKDRYGETSR
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RLSSYRLHQKTHSKQKRGSSKYKNALTCSLDVSHLTTRDERKHLHCNQCGKNFSCKS
YAIEHQRIHTGEKFYKCTRCKTFRWKSNFSRHMKLHKEVYKQEKRGEDFFKOSYQS
QVISTVEKTFPCQNCGKTFTQKKSLIEHQRIHTGEKFYQCSGCGETFTYRSSYIIHMK
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TREKPYQCRECEKAFRWSSNLYRHQRKHFLHKRYKYRESKETSNLQSKILIDQKPFWC
QECGKTFTRKRSLLDHKGIHSGERRFKCNLCEKSFDRNYRLVNHQRIHTTEQPQWRDK
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AQIWSPASHLKNSSALEDHLETSHGIGICDVLAEQTDSPAVSVPDYFQLEEGIEYQEA
LTFQDVEVTFSQEEWGCLNSAQRNLXXDVILENYGNVVSVVGSSPKPALISWLBARKP
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ESSKSIAFQNVPTKKKACHKCSTCGKTFKKHSHLISHKRCHTKERPFKCIVCGKTFRW
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RPGQELFRQLFRQLRYHESSGPLETLSRLQELCRWMRPDVLSKAQMLELLVLEQFLS
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/protein_id="AAQ24161.1"
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/mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (24-APR-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (bases 1 to 175440)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the entire insert Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
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----- Summary Statistics
Center project name: M_BA0438P19
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                       /rpt_family="L1" 3143. .3318
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1421. .1533
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7280. .7429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     '.pt_family="L2"
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11339.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13406
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10602. .1
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10453. .10584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="Alu"
10127. .10223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpt_family="MaLR"
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}._.5493
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7. .5282
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3. .13647
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                                                                                             family="ERVK"
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                                                                                                                                                                                                                                                                      tamily="Alu"
                                                                                                                                                                                                                                                                                                           family="Alu"
                                                                                                                                                                                                                                                                                                                                              family="ERV1"
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RESULT 8
AC094355
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Allen, C., Alten, H., Alsbrocks, S., Amin, A., Angulano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Baca, E., Baden, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagy, M., Forbes, L., Foster, M., Gubraratne, P., Haaland, W., Hamil, C., Houllins, Garner, T., Garza, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W.,
Gunaratne, P., Haaland, W., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muzny, D.Marie., Metzker, M.Lee., Abramzon, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
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28142
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22958. .23159
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3. .28352
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Pred. No. 3.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
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*** SEQUENCING IN PROGRESS ***,
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Nwackelemeh, C., Okwount, G., Olarinpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L. L., Pluzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regiar, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Trajor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, Q., Wang, S., Warren, R., Wei, X., Wei, X., White, F., Willama, G., Wilson, R., Wleczyk, R., Woden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstcok, G. and Gibbs, R.A.
                                                                                                                                                                                                                           contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                and, whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 9, 2003 this sequence version replaced gi:24942540. This sequence version replaced gi:24942540. This sequence version replaced gi:24942540.
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                                                                                                                                                                         table.
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----- Genome Center
Center: Baylor College of Medicine
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TITLE JOURNAL REFERENCE

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE AUTHORS TITLE

JOURNAL

Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu

Center project name: GALD
Center clone name: CH230-3C12
Center clone name: CH230-3C12
Center clone name: CH230-3C12
Center clone name: CH230-3C12
Assembly program: Atlas;
Consensus quality: 199312 bases at least Q40
Consensus quality: 201330 bases at least Q30
Consensus quality: 202750 bases at least Q20
Estimated insert size: 207083; sum-cf-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as

the gaps are

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AC132091
AC132091.3 · GI:50839052
HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (29-AUG-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC132091
                                                                                   Center project name: M_BB0465H15
                                                                                                                          Web site:http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                            Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                  Direct Submission
Submitted (30-JUI-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Jul 30, 2004 this sequence version replaced gi:34495013.
                                                                                                                                                                                                                                                                                                          Wilson, R.K.
                                                                                                                                                                                                                                                                                                                         Submitted (06-SEP-2003) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 140256)
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                                                                                                                                                                                                                                                                                                                                                                                                                 Parkway, St. Louis, MO
3 (bases 1 to 140256)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson, R.K.
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Mammalia; Eutheria; Rodentia;
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be preserved
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204379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="CH230-3C12"
                                                      Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
                                     1. .140256
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19497: gap of unknown length
204378: contig of 184881 bp in length
204478: gap of unknown length
216833: contig of 12355 bp in length
216933: gap of unknown length
218326: contig of 1393 bp in length.
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ne 18 clone RP24-465H15, complete sequence.
                                                                                                           Information
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AC016256/c
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                                                                                           Mammalia; Butheria; Primates; Caraniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(CE) 1 (bases 1 to 16405)

RS Murny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are-J.R., Banks, T., Babbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Boock, J., Chen, G., Chen, G., Chen, S., Daviett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carrer, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., C
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Homo sapiens 12 BAC RP11-98B6 (Roswell Park Cancer Institute
BAC Library) complete sequence.
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/chromosome="18"
/clone="RP24-465H15"
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100.0%; Pred. No.
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Mismatches
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Worley, K.C Direct Sub

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to (EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are c sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Direct Submission
Submitted (11-JUL-2001) Human Genome Sequencing
of Molecular and Human Genetics, Baylor College
Of Molecular and Human Genetics, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (24-NOV-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 164405)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (25-JUL-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Baylor Plaza, Houston,
4 (bases 1 to 164405)
                                                                                                                                                                                                                                                                                                                                                                                        QUALSTAT-REPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reports of lowest quality individual bases and measures quality are listed below. Description of the metrics can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Overlapping clones are noted at the beginning and Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Jul 11, 2001 this sequence version replaced gi:12656764 INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley, K.
                                                                                                                                                                                                                                                                                                                                                                                                                           http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gc-help@bcm.tmc.edu
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                                                                         /rpt_family="L1MA8"
2142. .2281
                complement (2827)
                                                                                                                                                                                                                     /clone="RP11-98E6"
complement(1. .371)
                                                                                                                     /note="Overlaps bases 186760. .191923 of clone AC087886"
/function="Overlaps with adjacent clone AC087886"
complement (439. .637)
                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="12"
                                                            , zpt
                                                                                                                                                                                                  , rpt
                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
      family="MIR"
                                                            _family="MIR"
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7825. .8933
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5502. .5527
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/rpt_family="L2"
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7163. .7191
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7069. .7153
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7015. .7068
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10582. .11009
                                                                               'note="CA or TG"
'function="Polymorphic site"
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4397. .14398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (07-AUG-2001) European Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, (E-mail: barrell@sanger.ac.uk) and Unite de Biochimie Physiologique, Universite Catholique de Louvain, Place Croix du Sud 2-20, B-1348 Louvain-la-Neuve, Belgium On Aug 9, 2001 this sequence version replaced gi:11967804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               see http://www.sanger.ac.uk/Projects/L_major/
CDS are numbered using the following system eg P696.01. P696
(cosmid name), .01 (first CDS)
To make the PAC library Leishmania major Friedlin DNA was partially
digested with NotI prior to cloning into the NotI site of the PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ivens,A.C., Lewis,S.M., Bagherzadeh,A.,
Smith,D.F.
                                                                                                                                                                               the Hexamer program which was written by Richard Durbin as an integral part of the ACEDB-based analysis tools for the C.elegans Genome Sequencing Project. The program calculates the log-likelihood score for a given DNA segment based on the frequency of 6-mers, normalised for the base-pair composition of the genome. The program was trained using a fasta file of confirmed Leismania major coding sequences (CDS), i.e. from ATG start codon to the stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS. Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. Gene prediction is done using:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Notes:
Details of leishmania sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Masuy,D., Purnelle,B., Goffeau,A., Ivens,A.C., Quail,M., Rajandream,M.A. and Barrell,B.G.
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Leishmania major Friedlin chromo
Where possible we choose an initiation codon (atg) which is preceded by a stretch of pyrimidines or part of a Kozak sequence. If this cannot be identified we choose the most upstream initiation codon. Transmembrane domains were predicted as implemented at the TMHMM server: http://www.cbs.dtu.dk/services/TMHMM-1.0/IMPORTANT: This sequence MAY NOT be the entire insert of the
                                                                                                                                                                                                                                                                                                                                                                  the FramePlot program of Bibb et al., Gene 30:157-166(1984) as implemented at http://www.nih.go.jp/~jun/cgi-bin/frameplot.pl. codon preference based on the codon usage table for http://www.kazusa.or.jp/codon/
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                                                                                                                                     CAUTION: We may not have predicted the correct initiation codon.
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Query Match
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Location/Qualifiers
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                                                                                                   Submitted (27-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On Jul 30, 2003 this sequence version replaced gi:32261442
                                                                                                                                                                                                                                                                                          Submitted (26-JUN-2003)
Parkway, St. Louis, MO
5 (bases 1 to 175062)
                                                                                                                                                                                                                          Submitted (30-JUL-2003)
Parkway, St. Louis, MO (
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (bases 1 to 175062)
McPherson, J.D. and Wat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence of Mus musculus Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shah, N.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Direct Submission
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                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                 Parkway, St.
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                                                                                                                                                                                                                                                                                                                                                                                    (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 175062)
Contact: submissions@watson.wustl.
----- Summary Statistics
Center project name: M_BB0115J20
                                              Center: Washington University Genome
Center code: WUGSC
Web site: http://genome.wustl.edu
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/strain="Friedlin"
/db_xref="taxon:5664"
/chromosome="14"
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1 to 175062)
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chromosome
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This sequence

may not represent the entire insert of this

clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions. repeat_region repeat_region /rpt_family="L1"
18263. .18690
/rpt_family="ERVK"
19452. .19708

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

# MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu

# SOURCE INFORMATION:

The RPCI-24 BAC Library has been constructed by Pietrer de Jong and coworkers (http://www.chori.org) from male C57BL/GJ mouse spleen and/or brain genomic DNA. The clone and detailed information can obtained from Pieter de Jong and coworkers at http://www.chori.org

# NEIGHBORING SEQUENCE INFORMATION:

FEATURES

This sequence is the entire insert of the clone. This clone is overlapped by AC131796 and AC117191.

Location/Qualifiers

## source /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" /chromosome="18" map="18"

4050 g T /clone="RP24-115J20" /clone_lib="RPCI-24" ğ _family="Alu" _family="ERV1" _family="L1" _family="Alu" _family="L1" _family="ERVK

repeat_region /rpt_family="L1" 13297. .13771 4804 _family="ERVK" _family="ERVK" _family="L1" _family="L1" _family="ERVK family="ERVK family="L1" family="ERVK" family="ERVK" .11619

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/rpt_family="ERVL" 13772. .14140

family="L1"

rpt_family="B4"

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50087. .5010" 34418 fami /rpt_family="B2"
33168. 337. /rpt_fami 41760..4 /rpc 1 /rpc 46075 49400 /rpt_family="B2" 46787. .46896 45830 42404 rpt_family="L1" 1201. .31495 rpt_fami family="L1" 1. .30039 _fami _fami _fami _family="ERVK" _fami _fami _tami family="L1" ). .49854 }. .47812 _family="B2" fami tam £ami fami family="L1" fami fami family="Alu" family="Alu tam: family="L1" fami family="MaLR family="B2" family="MaLR fam: family="B2" .49484 .49034 .44822 .29029 .48062 .46019 .34352 .42444 .34886 .30382 24356 21462 46440 22679 1y="L1" ly="L1" ly="L1" .ly="ERVK" .ly="B4" .1y="B4" ly="L1" ly="Alu" ly="B2" ly="ERVL" 1y="84" 3612 ly="ERVK" 1y="B4" ly="MaLR ly="L1" ly="ERVK ly="ERV1" ly="ERV1"

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REFERENCE
AUTHORS
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Ruzny, Marie, Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Allen, C., Allen, H., Alsbrooks, S., Anin, A., Angulano, D., Barder, M., Barnstead, M., Benahmed, F., Biswalo, K., Bair, J., Blankenburg, K., Blyth, P., Brown, M., Chen, S., Ch
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Submitted (15 NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Gon Nov 15, 2002 this sequence version replaced gi:23270014. On Nov 15, 2002 this sequence version replaced gi:23270014. On Nov 15, 2002 this sequence version replaced gi:23270014. On Nov 15, 2002 this sequence version replaced gi:23270014. On Nov 15, 2002 this sequence version replaced gi:23270014. On Nov 15, 2002 this sequence in the sequence in this seguence in the sequencing reads assemble dusing Atlas and whole genome shotgun sequence contigs are ordered and contig-scaffold, in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the Clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (Dases 1 to 229391)
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REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

TITLE JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

source * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/doce/Genbank draft data.)

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence be preserved as soon as it is available and the accession number will 10068 10168 30108 30208 219982 220082 Quality coverage: 8x in Q20 bases; sum-of-contigs estimation Center project name: GNVH Contact: hgsc-help@bcm.tmc Web site: http://www.hgsc.bcm.tmc.edu/ Center: Baylor College of Medicine Center code: BCM 224830 225856 225956 225957 Location/Qualifiers 10067: contig of 10067 bp in length
10167: gap of unknown length
30107: contig of 19940 bp in length
30207: gap of unknown length
219981: contig of 189774 bp in length
220081: gap of unknown length
224729: contig of 4648 bp in length
224829: gap of unknown length
224829: gap of unknown length
225855: contig of 1026 bp in length -- Genome Center Project Information contig of 1561 gap of unknown contig of 1775 gap of unknown length bp in length bp in length data.html).

FEATURES

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RESULT 14
AC142509
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       Baldwin, D. Bandaranaike, D. Barber, M., Barustead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M. L., Davis, C., Durp, A., Durbin, K., Duval, B., Eaves, K., Began, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Pranser, C., M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebrageorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gebrageorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hoyels, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idhein, R., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Johnson, 
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AC142509.1 GI:29501816
HTG: HTGS PHASE1; HTGS DRAFT.
Rattus norvegicus (Norway rat)
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Reeves, K., Regier, M.A., Reuter, M., Richards, S.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/db_xref="taxon:10116"
/clone="CH230-141P22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (03-APR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rose, M., Rose, R., Ruiz, S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 38 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 216536 bases at least Q40
Consensus quality: 221871 bases at least Q20
Consensus quality: 225261 bases at least Q20
Consensus quality: 225261 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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Center clone name: CH230-unknown
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    Summary Statistics

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29 TGCTGTTCTGCTGACTT 206145
Rattus norvegicus clone CH230-46A18, unordered pieces. AC097799
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20672
20772
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                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="CH230-unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
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20671: contig of 1737 b
20771: gap of unknown 1
24401: contig of 3630 b
24501: gap of unknown 1
26538: contig of 2037 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107470:
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71371:
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tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8: gap of unknown length
6: contig of 3878 bp in length
6: contig of 4280 bp in length
1: gap of unknown length
6: contig of 4285 bp in length
6: contig of 6395 bp in length
6: contig of 5655 bp in length
6: gap of unknown length
1: gap of unknown length
1: gap of unknown length
1: contig of 5618 bp in length
1: gap of unknown length
1: contig of 7388 bp in length
1: gap of unknown length
1: contig of 7888 bp in length
1: gap of unknown length
1: contig of 9958 bp in length
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                                                                                                      231140 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 231074;
                                                                                                         DNA
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RAILEN, Marie, Metaker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alabrooks, S., Amin, A., Angulano, D., Allen, C., Allen, H., Alabrooks, S., Amin, A., Barnet, B., Baden, H., Ballen, C., Allen, H., Alabrooks, S., Amin, A., Barnet, B., Baden, H., Ballen, C., Allen, H., Alabrooks, S., Amin, A., Barnet, B., Baden, H., Ballen, C., Baldwin, D., Bandaranaike, D., Barber, M., Barnet, B., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnet, B., Brown, M., Barnet, C., Chen, Z., Chu, J., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chu, J., Chacko, J., Chaver, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chaver, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chen, S., Deramo, C., Digy, K., Dinh, H., Dlyya, K., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Deramo, C., Digy, M., Chen, Y., Chen, Z., Chu, J., Chen, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Draper, H., Davy, K., Chen, Y., Chen, Y., Chen, Z., Chen, Y., Chen, Z., Chen, Y., Chen, Z., Chen, Y., Chen, P., Devak, M., Chen, Y., Ch
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 10, 2003 this sequence version replaced gi:24819446. The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                               Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                               Rat Genome Sequencing Consortium.
Direct Submission
                                                                                                                                                                                                                                    Baylor Plaza, Houston, 3 (bases 1 to 231140)
                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 231140)
Worley, K.C.
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34562 TGCTGTTCTGCTGACTT 34546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        table.
                                                                                                                                             Similarity
                                                            TGCTGTTCTGCTGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: GFGG
Center clone name: CH230-46A18
Center clone name: CH230-46A18
Center clone name: CH230-46A18
Center clone name: Atlas 3.0;
Assembly program: Atlas 3.0;
Consensus quality: 218455 bases at least Q40
Consensus quality: 220334 bases at least Q20
Consensus quality: 222131 bases at least Q20
Estimated insert size: 231276; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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228537
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                          clone_end:Sp6
site:EcoRI
                                                                                                                                                                                                                                                                                                                                              end_sequence:BH328184"
complement(227335..228129)
/note="clone_boundary"
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clone_end:T7
site:EcoRI
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db_xref="taxon:10116"
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                                                                                                               94.4%; Score 17; DB 2;
100.0%; Pred. No. 13;
tive 0; Mismatches
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Copyright (c) 1993 - 2005 Compugen Ltd.
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CB862324 HH05G12y
CL786064 OR BBa010
CC046788 3591 1 19
CL658930 OR CBa009
CL795021 OR CBa009
AQ689332 nbxxb0011D
CL615769 OR BBa000
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AQ689711 nbxxb00080P
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BM932647 UI-M-CGOP		CR155347 Reverse 8	GAKDUU	CDA	-				_				•	-	-	_		Mue		

ALIGNMENTS

## TITLE JOURNAL COMMENT ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS LOCUS DEFINITION RESULT 1 CB867772 FEATURES source Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum. 1 (bases 1 to 670) 1 (bases 1, Zhang, H., Burton, R., Stein, N., Langridge, P. and Grance A. Email: stein@ipk-gatersleben.de Insert Length: 670 Std Error: Plate: 1 row: D column: 6 Molecular Markers Group, Department Genbank Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstr. 3, 06466, Gatersleben, Germany Tel: 039482-5522 Barley ESTs from coleoptile tissue Unpublished (2003) Contact: Stein Nils HC01D06w CH Hordeum vulgare Sequence. CB867772 CB867772 Seq primer: CB867772.1 fordeum vulgare 039482-5595 /clone lib="CH" /clone lib="CH" /note="Vector: pSPORT; Site 1: SalI (5-end of cDNA); Site 2: NotI (3-end of cDNA); Due to the cloning system used blue/white selection for recombinants is not 100% reliable. Average insert size is 1.3 kb." /clone="HC01D06" /tissue_type="coleoptile" /dev_stage="coleoptile, 3 days old" /lab_host="DH1OB" Location/Qualifiers /organism="Hordeum vulgare" /mol_type="mRNA" /cultivar="Sloop" db_xref="taxon:4513" db_xref="GABI:531307" 670 bp mRN*I* Hordeum vulgare cDNA clone GI:30069748 .670 0.00 mRNA linear EST lone HC01D06 5-PRIME, EST 03-JUL-2003 IME, mRNA

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CBa002

Query Match

13.5%;

Score

67;

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Length 670;

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CB862324
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CL786064 793 bp DNA line OR BBa0103K12.f OR_BBa Oryza rufipogon genomic 5', genomic survey sequence.
CL786064
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Unpublished (2003)
Contact: Stein Nils
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 598)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: stein@ipk-gatersleben.de
Insert Length: 598 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular Markers Group, Department Genbank Institute of Plant Genetics and Crop Plant Research Corrensstr. 3, 06466, Gatersleben, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Graner, A
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Varshney,R.K., Zhang,H., Burton,R.,
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primer: SP6.
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039482-5595
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/dev stage="coleoptile, 1 day
/lab host="DH10B"
/clone_lib="HH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mol_type="mRNA"
cultivar="Sloop"
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clone="HH05G12"
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0; Mismatches
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CC046788/c
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Oryza rufipogon
Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 793)
                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1. (bases 1 to 539)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
INSERT LENGTH: 161 Std Error: 0.00
Plate: 0103 row: K column: 12
Seg primer: TAA TAC GAC TCA CTA TAG C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson,
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                 Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                                                                  CC046788.1
GSS.
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 Plate: 3591_1_190_1 row: 33 Class: transposon-tagged.
                                                Tel: 650 723 2227
Fax: 650 725 8221
                                                                                855 California Ave,
                                                                                                   Stanford University
                                                                                                                                                Maize genomic sequences found using Unpublished (2001)
                                                                                                                                                                                  Walbot, V.
                                                                                                                                                                                                                                                                   Zea mays
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Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OMAP Project
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                                walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBA"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA'
/db_xref="taxon:4529"
/clone="OR_BBa0103K12"
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/mol_type="genomic DNA"
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                                                                                  Palo
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Pred. No.
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                                                                                  Alto,
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Best Local S
Matches 29
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaae; Oryza.

1 (bases 1 to 733)
Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR_CBa0090A04.r OR_CBa Oryza
3', genomic survey sequence.
CL858930
CL858930.1 GI:51270762
                                                                                                                                                                                                                                                                                                                                                                                    OMAP project (2004) Unpublished (2004) Contact: Rod A. Wing Arizona Genomics Institute University of Arizona
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                                                                                                                                                                                       BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0090 row: A column: 04
Seg primer: CAC TCA TTA GGC ACC CCA
                                                                                                                                                                                                                                                                              Email: http://genome.arizona.edu
PCR PRimers
                                                                                                                                                                                                                                                                                                                   Tel: 520 626 9595
Fax: 520 621 1259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib=3591 - RescueMu Grid P"
/clone lib=3591 - RescueMu Grid P"
/note="Organ: leaf; Vector: RescueMu (engineered from
/note="Organ: leaf; Vector: RescueMu; Site_2: BglII;
pBlueScript backbone); Site 1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified malze Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid P was grown at Molokai in 2002. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
                                                                                                                                                                          BAC ends
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/lab_host="DH10B"
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/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
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/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_CBB0090A04"
/clone="CBC_CB0090A04"
/tissue_type="young leaves"
/dev_stage="2 week old seedlings"
                                                                                                                                                  ocation/Qualifiers
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Pred. No.
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clone OR_CBa0090A04
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RESULT 7 AQ689332/c

AQ689332

576 bp

DNA

linear

GSS 01-JUL-1999

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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, Ai
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 470 ATCGGTAATAAAAGGTGGCCCAAAGT 495
365
                             470 ATCGGTAATAAAAGGTGGCCCAAAGT 495
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3', genomic survey sequence.
CL795021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza rufipogon
Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
                                                                 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: http://genome.arizona.edu
ATCGGTAATAAAAGGTGGCCCAAAGT 340
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                                                                 Conservative
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/clone lib="OR_CBa"
/note="Vector: pAGIBAC1; Site_1: HindIII;
drk treated 36 hrs before harvest"
                                                                                                                                              /tissue_type="young leaves"
/dev stage="2 week old seedlings"
/lab_host="DH10B T1 phage resistant"
/clone_lib="OR_CBa"
/clone_lib="OR_CBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
drk treated 36 hrs before harvest"
                                                                                                                                                                                                                                                              /organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
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                                                                                                                                                                                                                                               clone="OR_CBa0004L03"
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                                     5.2%; 5.20
100.0%; Pred. No.
100.0%; Mismatches
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l00.0%; Pred. No.
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e OR_CBa0004L03
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.

1 (bases 1 to 576)
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                                                                               AQ255572 617 bp DNA linear GSS 23 nbxb0011D02r CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0011D02r, genomic survey
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A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nbxb0079G12f CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0079G12f, genomic survey
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Class: BAC ends
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Fax: 864 656 4293
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GSS.
                                sequence.
AQ255572
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  AQ255572.1 GI:3780054
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab host="E coli DH108"
//lab host="E coli DH108"
//clone lib="CUGI Rice BAC Library"
//note="Wector: pBeloBAC11; Site_1: HindIII; Site_2:
/note="Wector: populated messer populated nesser populated nesse
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
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Pred. No.
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0.028;
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LOCUS
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                                                                                                                  KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                        309
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Oryza rufipogon
Oryza rufipogon
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                     OR_BBa0008D16.r OR_BBa Oryza
                                                                                                                                                                      3', genomic survey sequence. CL615769
                                                                                                                                               CL615769.1
                                                                                                                                                                                                                                                              CL615769
                                                                                                                                               GI:49104999
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KEYWORDS
                                                    371 ATATGCTTGAGAAGAGAGTCGGG 393
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: GGAAACAGCTATGACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wing, R.A. and Dean, R.A.
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                                                                                                                                         Similarity
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ATATGCTTGAGAAGAGAGTCGGG 331
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864 656 4293
                                                                                                                                                                                                                                         /note="Vector: pBeloBakCl1; Site 1: HindIII; Site 2: /note="Vector: pBeloBakCl1; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the hund tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library form Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ity sequence stop: 296.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mol_type="genomic DNA"
cultivar="Nipponbare"
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                                                                                                                                      4.6%;
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                                                                                                                                      Score 23;
Pred. No.
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                                                                                                                                         DB 8;
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                                                                                                            0; Indels
                                                                                                                                                                Length 617
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bp DNA linear GSS 01-JUL-2004 rufipogon genomic clone OR_BBa0008D16

Mon Feb

14 10:13:00 2005

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VERSION
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AQ326905
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ORGANISM
                                FEATURES
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Best Local Similarity
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
In (bases 1 to 745)
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
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BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0008 row: D column: 16
Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
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Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U
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AQ326905.1 GI:4118755
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                                                                                                                                          Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cultivar-group) genomic
                              High quality sequence start: 4
High quality sequence stop: 316.
Location/Qualifiers
                                                                                       Seq primer: GGAAACAGCTATGACCATGClass: BAC ends
                                                                                                                                                                                                                                   Contact: Wing RA
                                                                                                                       Email: rwing@clemson.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="young leaves"
/lab_host="DH108-T1 phage resistant"
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/note="Vector:"pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza rufipogon"
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organism="Oryza sativa (japonica cultivar-group)"
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100.0%; Pred. No.
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                                                                                                                                                                                  29634, USA
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AQ689711
LOCUS
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Best Local (
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                                                                                                              source
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371 ATATGCTTGAGAAGAGAGTCGGG 393
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100 Jordan Hall, Cl
Tel: 864 656 7288
Fax: 864 656 4293
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nbxb0080M19f CUGI Rice BAC Library Oryza sativa (japonica
cultivar-group) genomic clone nbxb0080M19f, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
                                                                                                                                                                                                                                     Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
                                                                                                                                                                           High quality sequence stop: 279
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wing,R.A. and Dean,R.A. A BAC End Sequence the Rice Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ689711.1 GI:5330879
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23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab host="E. coli DH10B"
//clome lib="CUGI Rice BAC Library"
//clome lib="CUGI Rice BAC Library"
//clome lib="CUGI Rice BAC Library"
//note="Vector: pBeloBAC11; Site 1: HindIII; Site 2:
/note="Vector: pBeloBAC11; Site 1: HindIII; Rice is one of two most popular grains In the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 59.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
/organism="Oryza sativa (
/mol type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="nbxb0080M19f"
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
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lab_host="E. coli l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="nbxb0039P05r"
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                                                                                                                    (japonica cultivar-group)"
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AQ573760
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100 Jordan Hall, Cl
Tel: 864 656 7288
Fax: 864 656 4293
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 850)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ573760 850 bp DNA linear GSS 02-nbxb0084F24r CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0084F24r, genomic survey
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A BAC End Sequencing Framework to
Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ573760
AQ573760.1 GI:4974545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 310.
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/clone_lib="CUGI Rice BAC11; Site_1: HindIII; Site_2:
/note="Wector: pBeloBAC11; Site_2: HindIII; Site_2: HindIII; Site_2:
/note="Wector: pBeloBAC11; Site_2: HindIII; Site_2: HindIII; Site_2:
/note="Wector: pBeloBAC11; Site_2: HindIII; 
/db_xret="teavu...../
/clome="nbxb0084F24r"
/clome="nbxb0084F24r"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/lab_host="E. coli DH10B"
/clome lib="CUGI Rice BAC Library"
/clome="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
/note="Vector: pBeloBAC11; Site_1: HindIII; Rice is one of two most popular grains in the
HindIII; Rice is one of two most popular grains in the
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                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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100.0%; Pred. No.
tive 0; Mismatc
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OP_Ba0015P11.f OP_Ba Oryza
5', genomic survey sequence.
CW504264
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Seg primer: TAA TAC GAC TCA CTA TAG
Class: BAC ends.
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SanMiguel, P., Westerman, R., Kim, H., Yu, Y., Wissotski, M., Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.
OMAP Project - Purdue University
Unpublished (2004)
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                                                                                                                                                                                                                                                                                      BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161000 Std Error: 0.00
Plate: 0015 row: P column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: sjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with lucy version 1.19s.
Bases 27-880 of the raw sequence (length 1189) were retained after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           915 W. State St., West Lafayette, IN 47907, USA Tel: 7654963621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Scott A. Jackson Jackson Laboratory
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/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OP__Ba"
                                                                               /organism="Oryza punctata"
/mol_type="genomic DNA"
/db_xref="taxon:4537"
/clone="OP__Ba0015P11"
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Live 0; Mismatches
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100.0%; Pred. No.
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genomic clone
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OP__Ba0015P11
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Best Local S
Matches 23
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Best Local S
Matches 22
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                                                                                                                                                                     Local Similarity
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Unpublished (2004)
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3', genomic survey sequence.
CW523527
CW523527.1 GI:53997749
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BACKWARD: CAC TCA TTA GGC ACC CCA
INSERT Length: 161000 Std Error: 0.00
Plate: 0049 row: I column: 20
Seq primer: CAC TCA TTA GGC ACC CCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: sjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived
from the raw sequence read by clipping with lucy version 1.19s.
Bases 55-655 of the raw sequence (length 1219) were retained after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 601)
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915 W. State St., West Lafayette,
Tel: 7654963621
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                                                                                                                                                                                                                             /organism="Oryza punctata"
/mol type="genomic DNA"
/mol type="genomic DNA"
/db xref="texon: 4537"
/clone="OP_Ba0049120"
/tissue_type="young leaves"
/lab host="DH10B-T1 phage resistant"
/clone_lib="OP_Ba"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
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100.0%; Pred. No. 1.4;
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Pred. No.
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0.38;
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AUTHORS
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SOURCE
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Search completed: February 10, Job time: 3370.47 secs
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 702)

Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,

Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OR_CBa0028M15.r OR_CBa Oryza rufipogon genomic clone OR_CBa0028M15
3', genomic survey sequence.
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CL812779.1 GI:51054117
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University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
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/Clone="OR_CBa0028M15"
/tissue_type="young leaves"
/dev_stage="2 week old seedlings"
/lab_host="DH10B T1 phage resistant"
/clone_1ib="OR_CBa"
/note="Vector: paGIBAC1; Site_1: HindIII; Site_2: HindIII;
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ALIGNMENTS

## REFERENCE AUTHORS VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION ACCESSION RESULT 1 AX342369 밁 ₽ á В Ś FEATURES Query Match Best Local S Matches 1183 TITLE JOURNAL 1183; 121 121 61 61 Sequence 8 from Patent EP1167531. ۰ μ for detection thereof patent: EP 1167531-A 8 02-JAN-2002; Monsanto Technology LLC (US) Location/Qualifiers Behr, C.F., Hironaka, C., Heck, G.R. and You, J. Corn transformant py-zmgt32 (nk603) and comp synthetic construct AX342369.1 other sequences; artificial sequences. synthetic construct Similarity GACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGC GTTACTAGATCGGGGATATCCCCCGGGGAATTCGGTACCAAGCTTTTATAATAGTAGAAAA GTTACTAGATCGGGGATATCCCCGGGGAATTCGGTACCAAGCTTTTATAATAGTAGAAAA 180 GACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGC 100.0%; Score 1183; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches /organism="synthetic construct" /mol_type="unassigned DNA" /db xref="taxon:32630" /note="1-164 Agrobacterium tumefaciens nos 3' terminator 165-381 construct vector DNA 382-686 Zea maize plastid genes, rps11 and rpoA 687-1183 Zea maize genomic DNA" GI:18151812 DNA BB 6 <u>;</u> compositions Length 1183; Indels linear PAT 12-JAN-2002 and 0 methods Gaps 120 120 60 60 0

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                                                    RESULT 3
CHZMRPOA/C
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chloroplast Zea mays
Zea mays
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 CHZMRPOA 1627 bp Zea mays chloroplast rpoA gene: X07810. GI:12466
RNA polymerase alpha-subunit; rj chloroplast Zea mays
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ribosomal prote
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89193772
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1 (bases 1 to 721)

1 (bases 1 to 721)

1 (Markmann-Mulisch, U. and Subramanian, A.R.

Nucleotide sequence of maize chloroplast rpS11

acid sequence between eukaryotes, bacteria and Biochem. Int. 17 (4), 655-664 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Original
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                                                                                                                                                                TTGCAAACCCACTGTACGAATAGCATCTACTGCTGTTCT
                                                                                                                                                                                                    AATGGCTCGTAATGCGGCATCTCTTCCGCTACCAGCACCTTTTACCATAACTTCTGCTCG
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                                                                                                                                                                                                                                                        TCCATTATGCGGCATAGGTGTTACATCGCGTATACAACTTAACCGTACACCACTTTAGC
                                                                                                                                                                                                                                                                       TCCATTATGCGGCATAGGTGTTACATCGCGTATACAACTTAACCGTACACCACTTTTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Zea mays"
/organelle="plastid:chloroplast"
/mol_type="genomic DNA"
/db xref="taxon:4577"
200. .631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MTKAIPKIGSRKKVRIGLRRNARFSLRKSARRITKGIIHVQASF
NNTIITVTDPQGRVVFWSSAGTCGFKSSRKASPYAGQRTAVDAIRTVGLQRAEVMVKG
AGSGRDAALRAIAKSGVRLSCIRDVTPMPHNGCRPPKKRRL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source text: Maize chloroplast Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /proteIn_id="AAA84494.1"
/db_xref="GI:552742"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MVREEITGS"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAA84495.1"
/db_xref="GI:342629"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="rpoA gene product"
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100.0%; Pre
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0; Mismatches 0
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a; Poales; Poaceae; PACCAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-MAY-1988) H. Koessel, Institut fuer Biologie III Universitaet Freiburg, Schaenzlestr. 1, D-7800 Freiburg, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Structure and expression of the of DNA-dependent RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88289331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koessel,H.
                                                                                                                                                                                                               CGTCTTTTTTAGGAGGTCGACATCCATTATGCGGCATAGGTGTTACATCGCGTATACAA
                                                                                                                                                                                                                                                                                                                          CCTTTTACCATAACTTCTGCTCGTTGCAAACCCACTGTACGAATAGCATCTACTGCTGTT
                            CCTTTTACCATAACTTCTGCTCGTTGCAAACCCACTGTACGAATAGCATCTACTGCTGTT
                                                                                                CTTAACCGTACACCACTTTTAGCAATGGCTCGTAATGCGGCATCTCTTCCGCTACCAGCA
                                                                                                                      CTTAACCGTACACCACTTTTAGCAATGGCTCGTAATGCGGCATCTCTTCCGCTACCAGCA
                                                                                                                                                                                                                                                                             (bases 1 to 1627)
                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="Myrepitgstotlewkcvesrvdskrlyygrfilsplrkgoadt
VGIALRRALLGBIEGTCITRAKFGNVPHEYSTIVGIEBSIOETLANLKEIVLASNLYG
VRDASICVKGPRYITAODIILPBSVBIDDTCPIANLERDVDFCIELQIKRDRAKHTE
LRKNGODGSVED DAVEPVRNVNYSIFSCHORDEKHBILFLBIWTNGKLTPKBGGIYE
ASRNLIDLFLPFLHTBEBGTSFEENKARLTPPLLTFQKRFTNLKKNKKGIPLNCIFID
OLELBBRTYNCLKRANIPSALLDLLVKTEEDLIKINSFGMEDGKLIWDTLEKHLPIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=3
/transE_table=1
/product="rps11 protein (1
/protein_id="CAA30669.1"
/db_xref="GI:829328"
/db_xref="GI:829328"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="RNA polymerase alpha-subunit (AA 1-341)"
(protein id="CAA30670.1"
/db_xref="GOA:P09562"
/db_xref="UniProt/Swiss-Prot:P09562"
/db_xref="UniProt/Swiss-Prot:P09562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RDAALRATAKSGVRLSCIRDVTPMPHNGCRPPKKRRL"
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/clone="pzmc 303"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="GOA:P09561"
/db_xref="UniProt/Swif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mol_type="genomic DNA"
strain="Inrakorn"
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'translation="PPQYCGFKSSRKASPYAGQRTAVDAIRTVGLQRAEVMVKGAGSG
                                                                                                                                                                                     TTTAGGAGGTCGACATCCATTATGCGGCATAGGTGTTACATCGCGTATACAA
                                                                                                                                                                                                                                                                                                                                                                                          20.5%;
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Pred. No. 5.1e-129;
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The maize plastid psb8-psbF-petB-petD gene cluster: spliced and unspliced petB and petD RNAs encode alternative products Curr. Genet. 12 (1), 69-77 (1987) 88210525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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X86563
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Characterization of the mRNA transcripts of the 5-bisphosphate carboxylase, large subunit gene plant Mol. Biol. 4, 169-179 (1985)
                                                                                                                                                                                                               Two partially homologous adjacent light-inducible genes encoding polypeptides of the P700 chlorophyl complex of photosystem I 5. Biol. Chem. 260 (3), 1413-1421 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cotranscription and processing of 23S, 4.5S and chloroplasts from Zea mays Nucleic Acids Res. 12 (20), 7633-7647 (1984)
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Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6093045
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ADIKCIKIQIAGRLAGKEIARAECIKKGRLPLQTIRAKIDYCCYPIRTIYGVLGVKIW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             6415. 7141
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 Score 242;
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Best Local Similarity 100. Matches 242; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lilioppida; Poalee; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
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VENTLFEDGDGANTFRAFNPTQAEETYSMVTA VENTLFEDGDGANTFRAFNPTQAEETYSMVTA		KSIFLLKKENORLFRFLYNSYVSEYEFFLLFLRKOSSCLRLTSSGTFLERIIFSGKME	
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n_id="BAD27275.1"
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Best Local Similarity
Matches 202; Conserv
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                                                                                                                                                                                                                                                                                                  AMPA-N-acetyltransferase
Patent: US 6448476-A 27 10-SEP-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 2378)
Barry,G.F.
Plants and plant cells transformation
                                                                                                                                                                                                                                                                                                                                                                                Unclassified.
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              ACGCGGCCGCCCTAGGGATATC 364
                                                               ACTITATACCACCTTTTAACTGATGTTTTCACTTTTGACCAGGTAATCTTACCTTTGTTT
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                                                686
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ilarity 100.0%; Pred. No. 1.3e-105;
Conservative 0; Mismatches 0;
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complement(join(13649. .13696,14395.
/gene="trnG"
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/note="codon recognized: AUG; fMet"
complement(join(13649. .13696,14395.
                                                                                                                                                                                                                                                                                          1. .2378
                                                                                                                                                                                                                                                                /organism="unknown"
/mol_type="genomic DNA"
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AX044094/c
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Oryza sp.
Oryza sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Vagnoliophyta; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Patent: WO 0066748-A 49 09-NOV-2000;
ZENECA LIMITED (GB)
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AX044144
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                                                                                                                                         Patent: WO 0066747-A 44 09-NOV-2000;
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14.5%; Score 171; DB 6; 1 llarity 100.0%; Pred. No. 1.7e-87; Conservative 0; Mismatches 0;
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/mol_type="unassigned DNA"
/db_xref="taxon:52841"
                                                                                                      Location/Qualifiers
1. .1501
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/mol_type="unassigned
/db_xref="taxon:52841"
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Submitted (29-OCT-2003) ARC Centre for Integrative Legume Research,
The University of Queensland, Room 213, John Hines Building (69),
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Lucia, QLD 4072, Australia
                 /trānblation="masngkkptvgngqnqhkgvndgfsyeimldntggngsmtlgsg
atfkaemnaavnrgnflarrgldfgsqkkatdydyigldyaatykqtasasgnsrlcv
ygwfqnrglngvplveyyiieDwvdwvpdaqgkmvtidgaqykifqmdhtgptinggs
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YSPVTEKHLI DGMTVRELCSAA I TMSDNTAANLLLTT I GGPKELTAFLHIMMGDHVTRL
DRWEPELNEA I PNDERDTTWPVAMATTLRKLLTGELLTLASRQQLI DWWEADKVAGPL
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ETFKQYFSVRQQKRTSGHITVSDHFKEWAKQGWGIGNLYEVALNAEGWQSSGVADVTL
                                                                                                                                                                     /gene="sXynA"
3800. .4513
                                                                                                                                                                                                                                                      /note="from rice actin gene; Act1"
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                                                                                                                                                                                                                                                                                                                                                                                                                           /product="beta-lactamase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="other DNA"
/db_xref="taxon:255329"
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                                                                 /protein_id="AAR29086.1"
/db_xref="GI:39636981"
                                                                                                   'product="Xylanase"
                                                                                                                                   note="synthetic xylanase"
                                                                                                                                                     'gene="sXynA"
                                                                                                                                                                                                                                                                                        note="T7 RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                           translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon start=1
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                                                                                                                     codon_start=1
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Sequence 3 from Patent WO0214524.
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                                                                               /note="Poly-A signal from the nopaline synthetase gene
from Agrobacteriu m tumefaciens"
7434. .8084
                                                                                                                            /note="AtH1
6401. .6672
                                                                                                                                                                                                                                   /translation="msiqhervalipepaarcleveahpetijkkvkdaedolgarvgy
| ieldlinsgkilespreerepmmstekvllcgavlsridagoedgrritaesqublve
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| drwedeelneaipuderdtimpvamattlrklltgelltlasrqolidmmeadkvagpl
                       /note="Hygromycin
9120. .9359
                                                                                                                                                          /note="Ubi-promoter from maize"
4921. .6400
                                                                                                                                                                                                      EIGASLIKHW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                     LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
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/db_xref="GI:19577679"
                                                                                                                                                                                                                                                                                                                                                       note="unnamed protein product; Beta-lactamase (AmpR)"
                                                                 note="First exon-intron combination from Ubi-maize"
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                                        Escherichia coli"
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14.5%;

Score 171;

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6,

Length 9359;

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Matches 171; Conser
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AX473364
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  Oryza sativa (japonica cultivar-group)
                                          AC091532.13
                                                                                     complete sequence.
                                                                                                           Oryza sativa chromosome
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Seeds B.V. (NL)
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6401. .6672
/note="Poly-A signal from the nopaline synthetase gene from Agrobacteriu m tumefaciens"
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/db xref="taxon:32630"
2941. .4920
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                                          gene
                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                     http://genemark.biology.gatech.edu/GeneMark/), and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M., Overton II, L.L., Tsitrin, T., Kin, M.M., Bera, J.J., Jin, S.S., Fadrosh, D.M., Tallon, L.J., Koo, H., Zismann, V., Hsiae, J., Blunt, S., Vanaken, S.S., Riedmuller, S.B., Utterback, T.T., Feldblyum, T.V., Yang, O.Q., Haas, B.J., Suh, B.B., Peterson, J.J., Quackenbush, J., White, O., Salzberg, S.L. and Fraser, C.M.
White, O., Salzberg, S.L. and Fraser, C.M. Salzberg, C.M. Salzberg, S.L. and Fraser, C.M. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (11-FEB-2003) The Institute for Genomic Research, 9 Medical Center Dr, Rockville, MD 2085, USA, rbuell@tigr.org On Jan 31, 2003 this sequence version replaced gi:24308660. Address all correspondence to:rice@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (31-JAN-2003) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA 5 (bases 1 to 147344)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (03-MAY-2001) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA (bases 1 to 147344)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan and Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky,
                                                                                                                                                                                                                                                             This BAC overlaps with rice BACOSJNBa0014G15 (AC090882) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-NOV-2002) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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1 (bases 1 to 147344)
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                                                                                                                                                                                                                     (japonica cultivar-group)"
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                                                       7545 bp
from Patent WO03078614.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AX840289 11643 bp | Sequence 11 from Patent W003078614. AX840289 AX840289.1 GI:39978688
                                                                                                                                                                                                                                                                                                                                                                                                         Bakker, H.A., Florack, D.E. and Bosch, H.J.
Gntii (udp-n-acetylglucosamine:beta-d mannoside
beta (1,4)-n-acetylglucosaminyltransferase iii) expression in plants
patent: WO 03078614-A 11 25-SEP-2003;
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                     ACTTTATACCACCTTTTAACTGATGTTTTCACTTTTTGACCAGGTAATCTTACCTTTGTTT 282
                                                                                                                                     TTTTATAATAGTAGAAAAGAGTAAATTTCACTTTGGGCCACCTTTTATTACCGATATTTT
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ACTITATACCACCTTTTAACTGATGTTTTCACTTTTGACCAGGTAATCTTACCTTTGTTT
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Search completed: February 10, 2005, 13:13:42 Job time : 7299.97 secs

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score greater than or equal to the score of the result being printed,
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ADC84543

AAT80052

AAQ12707

AAT80055

ABK11039

ABK10687
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Aat80053 Rice acti
Adg69892 Vector pr
Adg69905 Vector pr
Adg79330 Plasmid p
Adm88919 pp010.1 v
Adm88907 pTB-5 ve
Adg69894 Vector pT
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Aag12707 Rice acti
Aat80055 Rice acti
Abkili039 pVDH636 v
Abkil0687 Transform
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                                                                                                                                                  Adc84543 Rice acti
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4 U	1	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
δ.	3	63	67	68	68	68	68	68	83	68	68	68	89	68	83	83	83	83	68	68	68	68	68	83	68
12.4			13.5	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7
000	707	399	4032	13680	11643	7545	5395	5395	5387	5387	5345	5345	5338	5338	5338	5338	5337	5337	5337	5337	5327	5327	5295	5295	5277
4	Δ.	σ	N	12	10	10	11	6	11	δ	11	თ	11	11	σ	6	Ľ	11	თ	Φ	11	σ	1	o	11
NOT COROL	AAFACOR7	AAD28024	AAV23237	ADP73931	ACF58344	ACF58343	ADN88905	ADG69890	ADN88925	ADG69910	ADN88901	ADG69886	ADN88899	ADN88913	ADG69898	ADG69884	ADN88903	ADN88914	ADG69900	ADG69888	ADN88911	ADG69896	ADN88922	ADG69907	ADN88909
	Aaf80287 Nucleotid	Aad28024 Chimera o	Plasmid	Trasmid	MUCIECT	-		_	TIALG	Adgeyero vector pr		vector F	-orard 6		Adgeses vector pr	Vector	•	pius	Vector	VECTOR	T PIFTOL				Adn88909 pTP5-1 ve

## ALIGNMENTS

RESULT 1

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Key
misc_feature
                                                                                                                                                                                                                Zea mays.
Oryza sativa.
Synthetic.
Chimeric.
                                                                                                                                                                                                                                                            ds; rice actin 1 promoter; RA1; RA1 intron; chloroplast transit peptide gene; glyphosate resistance; corn; 5-enol-pyruvylshikimate-3-phosphate synthase; EPSPS; Hsp70 intron; transcriptional terminator; cauliflower mosaic virus 35S promoter; PV-ZMGT32; transgenic; nk603.
                 22-JUN-2000;
13-OCT-2000;
13-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                            ABK15244 standard; DNA; 498
                                                                                                                                                                                                                                                                                                                      Corn nk603 5' transgene/genomic sequence
                                                                                                                                                                                                                                                                                                                                                           ABK15244;
                                                                                                                              misc_feature
                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                        08-MAY-2002
(MONS ) MONSANTO TECHNOLOGY LLC.
                                                      15-JUN-2001; 2001EP-00202314
                                                                         02-JAN-2002.
                                                                                           EP1167531-A1.
                  2000US-0213567P.
2000US-0240014P.
2000US-0241215P.
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                          /*tag= a
/note= "Corn :
305. .349
                                                                                                                                /note= "Vector sequence" 350. .498
                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                  /*tag=
                                                                                                               'note= "Rice ACT1 sequence'
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                                                                                                                                                                    genomic sequence"
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Best Local S
Matches 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a DNA construct (I) comprising a first (FI) and a second (F2) expression cassette. FI of the DNA construct, in operable linkage, has rice actin 1 (RA1) promoter, RA1 intron, chloroplast transit peptide gene (II), glyphosate tolerant 5-enol-pyruvylshikimate-3-phosphate synthase (BPSPS) gene (III), and transcriptional terminator (IV), and F2 has cauliflower mosaic virus 35S promoter, Hsp70 intron, (II), (III) and (IV). Also included are two DNA sequences from corn plant them (used to detect transgene junction points). The construct is useful for producing a corn plant that tolerates application of glyphosate herbicide by transforming a corn cell with, selecting the corn cell into a fertile corn plant. The present sequence is the 498b amplicon consisting of corn genomic sequence, vector sequences and Rice ACTI promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Behr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel DNA construct useful for producing a corn plant that tolerates application of glyphosate herbicide, comprises two transgene express
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                                                                                                                                                                                                                                                                                                                                                                GAGGTAAACAGATCAGCATCAGCGCTCGAAAGTTTCGTCAAAGGATGCGGAAACTGTTTCC
                                                                                                                                                                                         CGGCCCACGCGTGGTACCAAGCTTGATATCCCTAGGGCGGCCGCGTTAACAAGCTTACTC
                                                                                                                                                                                                                                                                                                           AGCCGCCGTCGCCAGTTCCGCCAGACTCCTCCTCTCTCGGCATGAGCCGATCTTTTCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                         TCCAGGGTGAAGTATCAGAGGATTTACCGCCCATGCCTTTTATGGAGACAAGAAGGAGGGGAG
                                                                                                                                            GAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGGTAAGA
                                                                                                                                                                                                                                                            GCATTTCCAACCCTAGAGACGTGCGTCCCTGGTGGGCTGCTCGGCCAGCAAGCCTTGTAG
                                                                                                                                                                                                                                                                                                                                                 GAGGTAAACAGATCAGCATCAGCGCTCGAAAGTTTCGTCAAAGGATGCGGAACTGTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                         TCCAGGGTGAAGTATCAGAGGATTTACCGCCCATGCCTTTTATGGAGACAAGAAGGGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGGTGGCCCAAAGTGAA
                                                                                TTACCGGTCAAAAGTGAAAACATCAGTTAAAAGGTGTATAAAGTAAAATATCGGTAATAA
                                                                                                                                                                       CGGCCCACGCGTGGTACCAAGCTTGATATCCCTAGGGCGGCCGCGTTAACAAGCTTACTC
                                                                                                                                                                                                                                                                                         AGCCGCCGTCGCCATTCGGCCAGACTCCTCCTCTCTCGGCATGAGCCGATCTTTTCTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; 25pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; 114 C; 131 G; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 498; DB 6; 1
100.0%; Pred. No. 9.6e-246;
live 0; Mismatches 0;
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498
                          498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 498;
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RESULT 2 ABK15245/c ID ABK152

ABK15245

standard; DNA; 1183

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Sequence 1183

B₽;

295

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289 C;

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0 Other

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The invention relates to a DNA construct (I) comprising a first (F1) and a second (F2) expression cassette. F1 of the DNA construct, in operable linkage, has rice actin 1 (RA1) promoter, RA1 intron, chloroplast transit peptide gene (II), glyphosate tolerant 5-enol-pyruvylshikimate-3 phosphate synthase (EPSPS) gene (III), and transcriptional terminator (IV), and F2 has cauliflower mosaic virus 355 promoter, HB970 intron, (II), (III) and (IV). Also included are two DNA sequences from corn plant Pv-ZMGT32(hk603) of 498 or 1183bp, or primers and probes derived from them (used to detect transgene junction points). The construct is useful for producing a corn plant that tolerates application of glyphosate tolerance to application of glyphosate, and growing the corn cell into a fertile corn plant. The present sequence is the 1183bp amplicon consisting of the Agrobacteium transcriptional terminator sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-2000;
13-OCT-2000;
13-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                 Behr
                                                                                                                                                                                                                                                                                          Novel DNA construct useful for producing a corn plant that tolerates application of glyphosate herbicide, comprises two transgene express:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PV-ZMGT32; transgenic; nk603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chloroplast transit peptide gene; glyphosate resistance; corn; 5-enol-pyruvylshikimate-3-phosphate synthase; EPSPS; Hsp70 intron; transcriptional terminator; cauliflower mosaic virus 35S promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chloroplast transit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK15245;
                          vector sequences
                                                                                                                                                                                                                                                   Claim 3; Page 16-17; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1167531-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                           (MONS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rice actin 1 promoter; RA1; RA1
                                                                                                                                                                                                                                                                                                                                     2002-165871/22
                                                                                                                                                                                                                                                                                                                                                                 CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nk603 3' transgene/genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                            MONSANTO TECHNOLOGY LLC
                                                                                                                                                                                                                                                                                                                                                               Hironaka C,
                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0213567P.
2000US-0240014P.
2000US-0241215P.
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/note= "Vector
382. .686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Corn
687. .1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165. .381
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/note= "T-AGRTU.nos vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/note= "Corn genomic sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag=
                          corn
                                                                                                                                                                                                                                                                                                                                                                 Heck GR,
                          sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plastid genes rpsl1/rpoA partial sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intron;
                                                                                                                                                                                                                                                                                             comprises two transgene expression
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RESULT 3
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ADDIO17
AC ADDIO
XX ADDIO
XX ADDIO
XX Expr
XX Expr
XX CORI
XX Expr
Y Dr
Y Dr
Y Dr
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Best Local Similarity
Matches 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphonate herbicide tolerance; aminomethyl phosphonic acid; AMPA; AAT; acyltransferase; transacylase; recombinant plant; expression cassette; corn; tobacco; wheat; cotton; canonla; rice; chloroplast transit peptide; CTP; glyphosate oxidase; GOX; glyphosate oxidoreductase; phnO gene; self-fertilisation; hetero-fertilisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter
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                                                                                                                                                                                                                                                                                                                                          terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transit_peptide
             Disclosure; Page 167-169;
                                        Enhancing phosphonate herbicide tolerance in corn, tobacco, wheat, cotton, canola and rice plants involves transforming plants with phosphonate metabolizing genes encoding acyltransferase enzyme.
                                                                                                                                                                                                                                                                   25-MAY-2000
                                                                                                     P-PSDB;
                                                                                                                                                                                                          17-NOV-1998;
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                                                                                                                                                                            (MONS ) MONSANTO
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DB; AAY71251.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCGTGGTACCAAGCTTGATATCCCTAGGGCGGCCGCGTTAACAAGCTTACTCGAGGTCA
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                                                                                                                                                                                                          98US-0108763P
                                                                                                                                                                                                                                       99WO-US027152
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Targets the protein to an organelle, like chloroplast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Enhances
1440. .1667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/note= "plant functional heterologous promoter"
/66. 1423
/*tag= b
/*tag= b
                                                                                                                                                                                                                                                                                                                                                        product= "Escherichia coli modified P2A AMPA product= "Escherichia coli modified P2A AMPA acyltransferase (AAT) enzyme"

/function= "Transfers acyl group from an acylcarrier (CoA) to the free amino group of aminomethylphosphonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                   1668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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100.0%; Prr
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               179pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 118;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC The patent discloses a method for selectively enhancing the phosphonate CC herbicide tolerance in recombinant corn, tobacco, wheat, cotton, canola CC and rice plants, by transforming the plants with an expression cassette. CC It comprises of a structural DNA sequence, that encodes an aminomethyl CC phosphonic acid (AMPA) acyltransferase or transacylase (AAT), capable of CC transit peptide (CTP), that targets AAT to the chloroplast. Co-expression CC of glyphosate oxidase (GOX) gene, encoding glyphosate oxidoreductase, CC along with AAT provides the transformed plants with higher resistance to CC phosphonate herbicides the transformed plants with higher resistance to CC phosphonate herbicides. This method is useful for enhancing phosphonate CC and to prevent self-fertilisation and enhance hetero-fertilisation. The CC present DNA sequence is the expression cassette-3, comprising a plant CC coli phno coding region, encoding P2A AMPA acyltransferase (AAT) enzyme CC and plant operable termination sequences
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                                                                                                  29-JUL-1999;
29-JUL-1999;
21-DEC-1999;
21-DEC-1999;
21-DEC-1999;
21-DEC-1999;
21-DEC-1999;
                                                                                                                                                                                            29-APR-1999;
29-JUL-1999;
29-JUL-1999;
29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2378 BP; 604 A; 625 C; 552 G;
                                                                                                                                                                                                                                                                                                                                                                  Rice EPSPS; 5-enolpyruvylshikimate phosphate synthase; glyphosate resistance; herbicide resistance; transgeni expression construct; enhancer element; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC87194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC87194 standard; DNA; 1501
                                                                                                                                                                                                                                                              20-APR-2000; 2000WO-GB001573
                                                                                                                                                                                                                                                                                                                  WO200066748-A1
                                                                                                                                                                                                                                                                                                                                         Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                       Rice actin promoter
                                                                                                                                                                                                                                                                                        09-NOV-2000
                                                                           (ZENE )
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                                                                           ZENECA
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                                                                                                                                                       99GB-00017846.
99GB-00017847.
99GB-00030200.
                                                                           LTD.
                                                                                                                 99GB-00030204.
99GB-00030207.
99GB-00030209.
                                                                                                                                                                                              99GB-00017840
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                                                                                                                                                                                                                                       99GB-00009968
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                                                                                                                                                                                                                                                                                                                                                                                                                          enhancer element,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 101;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO:49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 597 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                    transgenic
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Novel polynucleotide encoding 5-enolpyruvylshikimate phosphate synthase,

WPI; 2000-687544/67.

Hawkes

TR,

Warner SAJ,

Andrews

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Bachoo

S

Pickerill

ΑP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
 29-APR-1999;
29-APR-1999;
29-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rice EPSFS promoter, genomic DNA encoding a rice EPSPS chloroplast translit peptide, genomic DNA encoding a EPSPS protein modified such that it is resisteant to glyphosate (AAC87189), and a transcriptional terminator. The glyphosate resistant EPSPS contains a region (AAB29793) containing two amino acid substitutions relative to the corresponding wild-type region (AAB29792). The invention also encompasses plant genomic EPSPS sequences identified via screening with a rice EPSPS intronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPSPS) genomic DNA (AAC87188). The invention also relates to an expression cassette comprising, in the 5'-3' direction, one or motranscriptional enhancer elements selected from AAC87190-C87196),
                                                                                                                                                                                                         glyphosate;
                                                                                                                                                                                                            5-enolpyruvylshikimate
glyphosate; ds.
                                                                                                                                                                                                                                                              Rice actin enhancer.
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                                                                     20-APR-2000; 2000WO-GB001572.
                                                                                                       09-NOV-2000
                                                                                                                                         WO200066747-A1
                                                                                                                                                                         Oryza sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resistance or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          produce transgenic plants e.g. banana, wheat, maize resistance or tolerance to glyphosate herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                standard; DNA; 1501
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                                                                                                                                                                                                                                                                                              (first
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99GB-00009967.
99GB-00009969.
99GB-00009972.
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    425
                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                            phosphate synthase; EPSPS; herbicide resistance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 70;
Pred. No.
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RESULT 6
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Best Local
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29-JUL-1999;
29-JUL-1999;
29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to an Oryza sp. 5-enolpyruvylshikimate phosphate synthase (EPSPS) gene. Vectors containing the gene may be used to produce plant tissues and fertile whole plants which are substantially tolerant or substantially resistant to glyphosate herbicide and to produce a herbicidal target which is used for high throughput in vitro screening of potential herbicides
                                                                                                27-SEP-2001; 2001US-0325607P
                                                                                                                                                           WO2003027257-A2
                                                                                                                                                                                                  expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1501 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polynucleotide encoding a 5-enolpyruvylshikimate phosphate synthase from rice is used for producing transgenic plants with enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hawkes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-DEC-1999;
21-DEC-1999;
                                      WPI; 2003-354651/33.
                                                                             (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                                    27-SEP-2002; 2002WO-US030895
                                                                                                                                        03-APR-2003
                                                                                                                                                                              Melanomys caliginosus.
                                                                                                                                                                                                                     Rice actin promoter encoding
                                                                                                                                                                                                                                         01-JAN-2004
                                                                                                                                                                                                                                                            ADC84543;
                                                                                                                                                                                                                                                                              ADC84543 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistance to glyphosate herbicide.
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                                                                                                                                                                                                                                                                                                                                810 TAAGATTACC
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                                                          Dietrich
                                                                                                                                                                                                  cassette;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 54; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Warner SAJ,
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                         (first entry)
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99GB-00017835.
99GB-00017836.
99GB-00017843.
99GB-00030202.
99GB-00030210.
99GB-00030212.
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                                                          Budziszewski GJ
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                                                                                                                                                                                                                      sequence
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exonuclease dor particular for

reproducing

and

predictably manipulating

gene expression

3'-5'

New isolated nucleic acid molecule encoding a polypeptide with a 3' exonuclease domain, useful in molecular biology and transformation,

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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to an invention that results in the expression of the endogenous nucleotide sequence in plant cell be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2181 BP; 602 A; 518 C; 430 G; 631 T;
   This sequence represents the promoter region from the rice actin-1 (RAcl gene. Cytoplasmic actin is a fundamental and essential component of the eukaryotic cell and cytoskeleton. In higher plant cells, a number of cellular processes, such as cytoplasmic streaming, extension growth and cell division are thought to involve the cytoskeletal actin protein. All of the studied plant actins consist of four exons of conserved length,
                                                                                                                                                                                                                                      ₩u R,
                                                                                                                                                                                                                                                                                                       05-JAN-1990;
18-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice actin 1 gene
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04-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT80052 standard;
                                                                                                                                                    Nucleic acid containing the promoter of the rice actin-1 gene direct efficient expression of foreign genes in rice.
                                                                                                                                                                                                     WPI; 1997-340996/31
                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                          US5641876-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Promoter; rice; actin 1 cytoplasmic streaming; c
                                                                                                                                                                                                                                                                                                                                                       27-OCT-1993;
                                                                                                                                                                                                                                                                       (CORR ) CORNELL RES
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                                                                                                                                                                                                                                      Mcelroy
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                                                                                                                    Col 33-36; 29pp; English
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(first entry)
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91US-00762680.
                                                                                                                                                                                                                                                                                                                                                       93US-00144602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gene;
cell di
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e; cytoplasm; cytoskeleton; extension growth;
division; RAc1; maize; Adh1 promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0 U;
                                                                                     from the rice actin-1 (RAc1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0 Other;
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RESULT 8
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        separated by 3 introns of variable length. In rice there are at least 8 actin-like sequences per haploid genome. RAc1 encodes a transcript that is relatively abundant in all rice tissues. This sequence is an example of a nucleic acid molecule of the invention. The nucleic acid molecules of the invention contain the RAc1 gene (or fragments) with promoter activity in monocotyledonous plants. The promoter is used to direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression of foreign genes in transgenic rice and other plants. The actin promoter is more efficient in rice transformation than previously proposed promoters (e.g. 5 times more active than the maize Adhl promoter) and has constitutive activity in space and time. (Updated on 2)
                                                                                                                                                                                                                                                                                                                                                                                                  24-OCT-2003
25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                     Rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                   exon
                                                                                                                                                                                                                                                                                                       Кеу
                                                                                                                                                                                                                                                                                                                           Oryza sativa;
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ12707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ12707 standard; DNA;
                                                misc_RNA
                                                                             misc_RNA
                                                                                                                                   misc_RNA
                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                              promoter
                                                                                                                                                                                                                                                                                                                                                 Promoter;
                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-1991
                                                                                                                                                                                                        repeat_region
                                                                                                   TATA_signal
                                                                                                                                                                                                                                                                                                                                                                      actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 806 TACTCGAGGTCATTCATATGCTTGAGAAGAGTCGGGATAGTCCAAAATAAAACAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              356 TACTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAAACAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAGATTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2199 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAAGATTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                transgenic plant; monocotyledonous;
                                                                                                                                                                                                                                                                                                                                                                   gene RAc1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                             variety IR26.
                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                     /*tag= h
                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                           /rpt_type= tandem (imperfect)
1352. .1386
               /label= genominc
1650. .1728
                                                                                                                                                                                                            /rpt_type= direct
1301. .1333
                                                                                                                                                                                                                                       /rpt_type= direct
1078. .1088
                                                 650. .3741
                                                                                                                                                       rpt_type= tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    603 A; 515 C; 446 G; 635 T; 0 U; 0 Other;
                                                                                           *tag=
                                                                                                                label=
                                                                                                                                                                                                  *tag=
                                                                                                                                                                                                                                *tag=
                                                             abel= transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.1%;
100.0%;
                                                                                                    .1617
                                                                                 .1653
"transcription initation site"
                                                                                                                                               "eight
                                                                                                               purine-rich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 70;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВР
                                                                                                                                            pentamers"
                               clone
                                                                                                                                                        (imperfect)
                                                                                                                region
                                                               initiation signal
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                               pRAc1
                                                                                                                                                                                                                                                                                                                                                   88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2199
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RESULT 9
AAT80055
ID AAT8
XX
AC AAT8
XX
DT 25-M
DT 04-N
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                                                                                                                                                                                                                                                                               Matches
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Best Local (
                                                                                                                                                                                                                                                                                                    of the translation initiation region. This 5' intron separates a 79 bp (-rich 5' noncoding exon from the exon coding the translation initiation codon. This is one of few cases of a 5'-noncoding exon in a plant gene. The promoter region can be used to confer high level expression of foreign genes in transgenic rice and other agronomically important plants. It is five times more active than the maize Adhl promoter in trans-formed rice. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                       screened with a heterologous actin probe. The CDS encodes a 377 amino acid actin protein of 41.9 kD. The gene is interrupted by three introns (position not disclosed). Analysis also revealed an additional intron 5'
  25-MAR-2003
04-NOV-1997
                                       AAT80055;
                                                                                                                                                                                                                                                                                                                                                                                                                                The seugence was obtd. from a clone isolated from a rice genomic library screened with a heterologous actin probe. The CDS encodes a 377 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice actin gene promoter - used to confer high level expression foreign genes in transgenic rice and other plants.
                                                             AAT80055 standard; cDNA; 5643 BP
                                                                                                                                                                                                                                                                             Sequence 5510 BP; 1466 A; 1262 C; 1163 G; 1619 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Page 10; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₩u R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUL-1991
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                                                                                                                             869
                                                                                                                                                    416
                                                                                                                                                                            809
                                                                                                                                                                                                     356
                                                                                                                                                                                                                             70;
                                                                                                                                                                                                                                          Similarity
                                                                                                                                                  TAAGATTACC 425
                                                                                                                                                                                                     TACTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGG
                                                                                                                                                                                                                            14.1%; So ilarity 100.0%; F Conservative 0;
(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-00461490.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= putative
1034. .2044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label= 5' acceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label= 3' donor splice site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note=
                                                                                                                            878
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== "GC-rich -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2012
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                                                                                                                                                                                                                            Score 70; DB; Pred. No. 1.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          branch point splice site
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                                                                                                                                                                                                                         DB 2; uc.
.o. 1.7e-25;
0;
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a 79 bp
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RESULT 10 ABK11039

ABK11039 standard; DNA; 9359

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698

878

416 TAAGATTACC

425

909 356

TACTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGG TACTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGG

Best Loc Matches Query Match

Local

Similarity

14.1%;

Score 70; Pred. No. Mismatches

DB 2; 1.7e-25; 0,

Length 5643 Indels

Gaps

415

Conservative

0;

05-JUN-2002

(first entry)

pVDH636 vector; circular; cyclic; grass; plant; herbicide baseball; cricket; football; golf; rugby; soccer; tennis;

resistance; lawn; park;

pVDH636 vector containing Arabidopsis AtH1 gene.

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of the studied plant actins consist of four exons of conserved length, separated by 3 introns of variable length. In rice there are at least 8 actin-like sequences per haploid genome. RAC1 encodes a transcript that is relatively abundant in all rice tissues. This sequence is an example of a nucleic acid molecule of the invention. The nucleic acid molecules of the invention contain the RAC1 gen. or fragments with promoter activity (see ANT80052) and ANT80053) in monocotyledonous plants. The promoter is used to direct expression of foreign genes in transgenic rice and other plants. The actin promoter is more efficient in rice transferration than promoter is more efficient in rice
                                                                                                                                                                                                                                                                    cellular processes, such as cytoplasmic streaming, extension growth and cell division are thought to involve the cytoskeletal actin protein. All of the studied plant actins consist of four avenual function protein.
                                    transformation than previously proposed promoters (e.g. 5 times more active than the maize Adhl promoter) and has constitutive activity is space and time. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                             This sequence represents a the rice actin-1 (RAc1) gene amplified using AAT80054. Cytoplasmic actin is a fundamental and essential component of the eukaryotic cell and cytoskeleton. In higher plant cells, a number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid containing the promoter of the rice actin-l direct efficient expression of foreign genes in rice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-340996/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JAN-1990;
18-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Promoter; rice; actin 1 gene; cytoplasm; cytoskeleton; extension growth; cytoplasmic streaming; cell division; RAcl; maize; Adhl promoter; ss.
Sequence 5643 BP; 1500 A; 1283 C; 1200 G; 1660 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Col 3-7; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wu R, Mcelroy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5641876-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rice actin 1 gene
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91US-00762680.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene -
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RESULT 11
ABK10687
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Best Local (
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27-NOV-2000;
27-NOV-2000;
22-JUN-2001;
                                                                                                                                                                                                                                The invention relates to a grass plant, which has been genetically modified to substantially inhibit generative propagation and carry herbicide resistance. The grass is useful for growth and/or propagation of grasses. The grass is used to play at least one sport (e.g. baseball, cricket, football, golf, rugby, soccer or tennis), or used at least in a portion of an athletic field, lawn or park. The grass is fed to animal (e.g. cattle, goat, horse or sheep) or used as an animal feedstuff. The present sequence represents the coding sequence of pVDH636 vector containing the Arabidopsis AtH1 gene, which was used to inhibit flowering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
Cauliflower mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agrobacterium tumefaciens.
Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       athletic field; animal feedstuff; grass flowering inhibitor; AtH1; gene; {f ds} .
                                                                                                                                                                                                                                                                                                                                                                                    New genetically modified grasses that express inhibited generative propagation, or herbicide resistance, useful for forage (e.g. cattle feedstuff) or amenity purposes (e.g. for use in an athletic field, li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-AUG-2001; 2001WO-EP009572
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           ABK10687
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                  Example 1;
                                                                                                                                                                                                                                                                                                                                                                                   propagation,
feedstuff) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ADVA-)
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                                                                   6748
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                                                                                       416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADVANTA SEEDS
                                                                                                                                                                    Similarity
                                                                                                                          TAAGATTACC
                                                                                                                                                                                                      9359
                                                                   TAAGATTACC
                                                                                                              TACTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGG
            standard;
                                                                                                                                                                                                                                                                                                                                                 Fig
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                                                                                                                                                       14.1%;
ilarity 100.0%;
Conservative (
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2000US-0253274P.
2000US-0253327P.
2000US-0300220P.
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/partial
/note= "No stop codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  56pp;
                                                                                                                                                                                                     2377 A;
            DNA;
                                                                   6757
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                                                                                                                                                                                                                                                                                                                                                                                   purposes
                                                                                                                                                                                                                                                                                                                                                  English.
              9359
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                                                                                                                                                                                                     2222 C;
                                                                                                                                                          <u>.</u>.
                                                                                                                                                         Score 70; DB; Pred. No. 1.7.
              ВÞ
                                                                                                                                                                                                                                                                                                                                                                                   (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smeekens
                                                                                                                                                                                                      2133
                                                                                                                                                                                                     G; 2624 T; 0 U; 3 Other;
                                                                                                                                                                    DB 6; Ld
1.7e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proveniers
                                                                                                                                                                               Length 9359;
                                                                                                                                                           Indels
                                                                                                                                                           0;
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                      lawn
                                                                                                                 6747
                                                                                                                                       415
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The invention relates to a grass plant which has been genetically comodified to substantially inhibit generative propagation. The genetic comodification may result in a heritable change in one or more plant characteristics such as inhibition of flowering (or substantial delay that amounts to inhibition), absence of inflorescence, increased componental switch from vegetative to generative growth. A method of committees with metabolism of gibberellic acid. A grass can be treated by interferes with metabolism of gibberellic acid. A grass can be treated by complying a phytohormone to at least partially relieve or reverse a change complying a phytohormone to at least partially relieve or reverse a change complying a phytohormone to at least partially relieve or reverse a change complying a phytohormone to at least partially relieve or reverse a change complying a phytohormone to at least partially relieve or reverse a change complying a phytohormone to at least partially relieve or reverse a change complying a phytohormone to at least partially relieve or reverse a change complying a phytohormone to at least partially relieve or reverse a change complying a phytohormone to at least partially relieve or reverse a change complying a phytohormone to at least of the grass is also useful as an animal feedstuff for cattle, goats, horses and sheep, due to its increased vegetative growth, improved digestibility can be grass in a sanimal feedstuff. This sequence represents components on truit and the propagation vector for production of transgenic grasses expressing the Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grass; plant; transgenic; flowering inhibition; inflorescence; gene; ds; tiller production; delayed heading; gibberellic acid; phytohormone; golf; genetically modified grass; athletic field; sport; baseball; cricket; football; rugby; soccer; tennis; lawn; landscaping; cattle; horse; sheep; goat; animal feedstuff; Arabidopsis thaliana; AtHI; homeobox gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New genetically modified grass useful for growing and/or propagating grass in athletic fields (for sports such as baseball, cricket, football, golf, rugby, soccer and tennis), or as animal feedstuff for cattle, goat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-AUG-2000; 2000US-0226422P.
27-NOV-2000; 2000US-0253274P.
27-NOV-2000; 2000US-0253327P.
22-JUN-2001; 2001US-0300220P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   circular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-AUG-2001; 2001WO-EP009570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK10687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 6; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-257603/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Van Der
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200214486-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ADVA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADVANTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU76885
gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cyclic; pVDH636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ש
    AtH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vector plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
4930..6351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΒV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CMP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVDH636 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smeekens SCM,
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TACTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGG

Query Match Best Local S Matches 70

Similarity

14.1%; llarity 100.0%; Conservative (

0

Mismatches

Score 70; Pred. No.

DB 6; 3. 1.7e-25; 0;

0

Gaps

415 0

Length 9359; Indels

Sequence

9359

B₽;

2377

A; 2222 C; 2133 G;

2624 T; 0 U;

3 Other;

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RESULT 12
ADG69912
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                                                                                                               Query Match
Best Local S
Matches 68
                                                                                                                                                                                               The present invention describes a transgenic plant (I) comprising an expression cassette with a promoter operably linked to a ferulic acid esterase encoding polynucleotide. Also described: (I) controlling (MI) the level of phenolic acids in plant cell walls of a transgenic plant by introducing into the plant an expression cassette comprising a promoter operably linked to a ferulic acid esterase encoding polynucleotide; and (2) a transgenic plant (II) produced by (MI). The transgenic plants are useful in improving digestibility for livestock and enhancing biomass conversion. The method is useful for enhancing the production of more highly fermentable carbohydrates in plants, especially forage grasses. The expression cassette is useful for controlling the level of phenolic acids in plant cell walls of a transgenic plant. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New transgenic plant comprising an expression cassette with a promoter operably linked to a ferulic acid esterase encoding polynucleotide, useful in improving digestibility for livestock and enhancing biomass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transgenic plant; ferulic acid es plant; cell wall; improved digest highly fermentable carbohydrate;
                                                                                                                                                                         Sequence 1259 BP; 337 A; 332 C; 268 G; 322 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn-Coleman N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2000; 2000US-0249608P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-NOV-2001; 2001WO-US043588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200268666-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG69912 standard; DNA; 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEMV ) GENENCOR INT INC.
                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8899
                            418
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                                                       16
76
                                                                                                                  68;
                                                                          CTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAAGATTACC 6757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGATTACC
                                                         CTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAAGATTACC
                                                                                                                                                                                                                                                                                                                                                                                                        Fig 50A-B; 208pp; English.
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Langdon
83
                            425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ferulic acid esterase; FAE; enzyme; phenolic improved digestibility; biomass conversion; carbohydrate; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotide sequence.
                                                                                                         13:7%; 500
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ħ,
                                                                                                               Score 68; DB; Pred. No. 2e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۳,
                                                                                                           DB 6; 4...
0. 2e-24;
0;
                                                                                                                                         Length 1259;
                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                controlling (M1)
transgenic plant by
                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid;
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6747
                                                       75
                                                                                                               0
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RESULT 14
AAT80053
ID AAT80
XX
AC AAT80
XX
AC AAT80
DT 25-MA
DT 04-NC
XX
DE Rice

AAT80053;

AAT80053 standard; cDNA; 1392 BP

25-MAR-2003 04-NOV-1997

(first (revised)

entry)

Rice actin 1

gene promoter fragment.

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RESULT 13
ADN88926
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                                                               S
                                                                                                                                    Matches
                                                                                                   Query Match
Best Local
                                                                                                                                                                 The present invention relates to transgenic plants comprising an expression cassette having a promoter operably linked to a ferulic acid esterase (FAE) encoding polynucleotide. The transgenic plants are useful for enhancing the availability of fermentable carbohydrates as feed for grass-fed animals. The methods are useful for reducing the levels of phenolic acids in the cell walls available for cross-linking either by directly disrupting ester bonds linking phenolics and lighins to cell wall polysaccharides or by preventing excessive ferulation of cell wall
                                                                                                                                    Sequence 1259 BP; 337 A; 332 C; 268 G; 322 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                    21-MAY-2002; 2002WO-US016239
                                                                                                                                                         carbohydrates. The present sequence was used to
                                                                                                                                                                                                                                                                     Disclosure; Fig 50; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-457563/43.
                                                                                                                                                                                                                                                                                                                                                                         Dunn-Coleman N,
                                                                                                                                                                                                                                                                                                                                                                                                                     16-NOV-2001;
16-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003043411-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actin promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADN88926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADN88926 standard; DNA; 1259
                                                                                                                                                                                                                                                                                                                                                                                                (GEMV ) GENENCOR INT INC.
                                                                                                Local
                                                                                                                                                                                                                                                                                             animals.
                                                        358 CTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGGTA
                     418 AGATTACC
76
                                           16 CTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGGTA
                                                                                         68;
                                                                                                   Similarity
 AGATTACC
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     2001US-00991209
2001WO-US043588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phenolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                         Langdon
                     425
 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ferulic acid esterase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                 13.7%;
                                                                                                                                                                                                                                                                                                                                                                         Ħ,
                                                                                        0
                                                                                                 Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВÞ
                                                                                                                                                                                                                                                                                                                                                                           Morris
                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                           ש
                                                                                                DB 11;
2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fermentable carbohydrate;
ter; ds.
                                                                                        0
                                                                                                            Length 1259;
                                                                                                                                                          illustrate the
                                                                                         Indels
                                                                                        0
                                                                                                                                                          invention
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                  useful
                                                                                                                                                                                                                                                                                                         grass
                                                                   417
                                            75
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RESULT 15
ADG69892
ID ADG69
XX ADG69
XX ADG69
XX ADG69
XX L1-M2
XX Vectc
XX Vectc
XX Lrans
KW Lrans
KW plant
KW highl
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a number of cellular processes, such as cytoplasmic streaming, extension a number of cellular processes, such as cytoplasmic streaming, extension growth and cell division are thought to involve the cytoskeletal actin protein. All of the studied plant actins consist of four exons of conserved length, separated by 3 introns of variable length. In rice there are at least 8 actin-like sequences per haploid genome. RAc1 encodes a transcript that is relatively abundant in all rice tissues. This sequence is an example of a nucleic acid molecule of the invention. The nucleic acid molecules of the invention contain the RAc1 gene (or fragments) with promoter activity in monocotyledonous plants. The promoter is used to direct expression of foreign genes in transgenic rice and other plants. The actin promoter is more efficient in rice transformation than previously proposed promoters (e.g., 5 times more active than the maize Adhl promoter) and has constitutive activity in space and time. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Promoter; rice; actin 1 gene; cytoplasm; cytoskeleton; extension growth; cytoplasmic streaming; cell division; RAc1; maize; Adh1 promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid containing the promoter of the rice actin-1 gene - used to direct efficient expression of foreign genes in rice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a fragment from the promoter region of the rice actin-1 (RAc1) gene. Cytoplasmic actin is a fundamental and essential component of the eukaryotic cell and cytoskeleton. In higher plant cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wu R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JAN-1990;
18-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUN-1997.
                  transgenic plant; ferulic acid esterase; FAE; enzyme; phenolic plant; cell wall; improved digestibility; biomass conversion; highly fermentable carbohydrate; gene; ds.
                                                                                                                            11-MAR-2004
                                                                                                                                                                                                ADG69892 standard; DNA; 3657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1392 BP; 376 A; 343 C; 309 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORR ) CORNELL RES FOUND INC
                                                                                         Vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1997-340996/31
                                                                                                                                                                                                                                                                                                                       418
                                                                                                                                                                                                                                                                                                                                                                                                358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Col 35-38; 29pp; English.
                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcelroy
                                                                                       pTP8-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                               CTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGGTA 417
                                                                                                                                                                                                                                                                                                                           AGATTACC 425
                                                                                                                                                                                                                                                                                                                                                           CTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGGTA
                                                                                                                                                                                                                                                                                      AGATTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                       nucleotide sequence.
                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90US-00461490.
91US-00762680.
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                                                                                                                                                                                                                                                                                        89
                                                                                                                                                                                                                                                                                                                                                                                                                               13.7%; Score 68; DB
100.0%; Pred. No. 1.9
tive 0; Mismatches
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                                                                                                                                                                                                                       introducing into the plant an expression cassette comprising a promoter operably linked to a ferulic acid esterase encoding polynucleotide; and (2) a transgenic plant (II) produced by (M1). The transgenic plants are useful in improving digestibility for livestock and enhancing biomass conversion. The method is useful for enhancing the production of more highly fermentable carbohydrates in plants, especially forage grasses. The expression cassette is useful for controlling the level of phenolic acids in plant cell walls of a transgenic plant. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New transgenic plant comprising an expression cassette with a properably linked to a ferulic acid esterase encoding polynucleots useful in improving digestibility for livestock and enhancing be
                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a transgenic plant (I) comprising an expression cassette with a promoter operably linked to a ferulic acid esterase encoding polynucleotide. Also described: (1) controlling (M1) the level of phenolic acids in plant cell walls of a transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 36B-E; 208pp;
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ALIGNMENTS

REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 1 BZ310383 LOCUS DEFINITION COMMENT FEATURES TITLE JOURNAL source BZ310383 537 bp DNA linear GSS 06-NOV-ic53c07.bl WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays genomic clone ic53c07 5', genomic survey sequence.
BZ310383 GI:24672266 GSS. Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Katzenburger, F., King, L., Miller, B., Muller, S., Zutavern, T., McCombie, W.R. and Marttenssen, R.A. High quality sequence stop: !
Location/Qualifiers Plate: ic53 row: c colur Seq primer: -21M13UnivFwd Tel: 516 367 8884 Fax: 516 367 8874 Contact: W. Richard McCombie Genomic shotgun sequences from Unpublished (2002) Zea mays Zea mays Email: mccombie@cshl.org Class: shotgun (bases 1 to 537) /clone="1c53cv."
/lab host="JMN07 or DH5a"
/lab host="JMN07 or DH5a"
/clone lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
/clone lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
/note="Organ: immature ears; Site_1 and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, .b/g reads in pUC19). The same /organism="Zea mays" /mol_type="genomic DNA" /cultivar="B73" /db_xref="taxon:4577" /clone="ic53c07" .537 column: 537. 07 Zea mays (methyl-filtered) Dedhia, N., Nascimento, GSS 06-NOV-2002

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LOCUS
DEFINITION
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                                                                                                                                                                   Email: mccombie@cshl.org
Plate: hw43 row: f column:
Seq primer: -21M13UnivFwd
Class: shotgun
                                                                                                                                                                                                                       Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
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Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
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hw43f05.g1 WGS-ZmaysF
genomic clone hw43f05
BH883307
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streprophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidaee; Andropogoneae; Zea.

1 (bases 1 to 553)
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/lab_host="JM107 or DH5a"
/clone lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
/clone="Organ: immature ears; Site_1: Xba I; Site_2: Xba 1
/note="Organ: immature ears; Bite_1 : Xba I; Site_2: Xba 1
The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic D
                                                                           /mol_type="genomic_DNA"
/cultivar="B73"
/db_xref="taxon:4577"
                                                                  /clone="hw43f05"
                                                                                                                 organism="Zea mays"]
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138
                                   686
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Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N. Katzenburger,F., King,L., Miller,B., Muller,S., Nasciment Zutavern,T., McCombie,W.R. and Martienseen,R.A. Genomic shotgun sequences from Zea mays (methyl-filtered) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. BZ314790 648 bp DNA linear Gi hz22a01.bl WGS-ZmaysF (JM107 adapted methyl filtered) genomic clone hz22a01 5', genomic survey sequence. BZ314790 BZ314790.1 GI:24683733 Email: mccombie@cshl.org Plate: hz22 row: a column: Seq primer: -21M13UnivFwd PO Box 100, Cold Tel: 516 367 8884 Fax: 516 367 8874 Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA High quality sequence stop: Location/Qualifiers Class: shotgun Contact: W. Richard McCombie Unpublished Zea mays Zea mays (bases 1 to 648) /mol_type="genomic DN /cultivar="B73" /db_xref="taxon:4577" 1. .648 organism="Zea mays" (2002) DNA" 648 ဌ Dedhia, N., Nascimento, GSS 06-NOV-2002 Zea mays

ORIGIN

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RESULT 4
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                                                                                                                      Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                    Email: mccombie@cshl.org
Plate: ig96 row: e colun
Seq primer: -21M13UnivRev
Class: shotgun
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/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleoTide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in M13mp19, .b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a. "
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1 (bases 1 to 717)
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                                Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874 Email: mccombie@cshl.org
                                                                                                                                                                                                                           Unpublished (2002)
Contact: W. Richard McCombie
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mccombie@cshl.org
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/clone_lib="WGS-ZmaysF (DH5a methyl filtered)"
/clone_lib="WGS-ZmaysF (DH5a methyl filtered)"
/clone_fib="WGS-ZmaysF (DH5a methyl filtered)"
/note="Organ; immature ears; Site 1: Xba I; Site 2: Xba I;
/note="Organ; immature ears; Site 1: Xba I; Site 2: Xba I;
/rhe vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (x/y reads in M13mp19, .b/g reads in pUC19). The same ligation was transformed into DH5a."
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/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
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Zea mays
Zea mays
                                                                      1 (bases 1 to 738)
Rabinowicz, P. D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Rabinowicz, P. D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zutavern, T., McCombie, W.R. and Martienssen, R.A.
Zutavern, T., McCombie, W.R. and Martienssen, R.A.
Genomic shorgun sequences from Zea mays (methyl-filtered)
                  Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome :
                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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ii76c10.b1 WGS-ZmaysF (DH5a methyl filtered)
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/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleoTide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, .b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a. "
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/cultivar="B73"
/db_xref="taxon:4577"
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tive 0; Mismatches 0;
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d) Zea mays genomic clone
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Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Katzenburger, F., King, L., Miller, B., Muller, S., Zutavern, T., McCombie, W.R. and Martienssen, R.A.
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Plate: ii76 row: c colu
Seq primer: -21M13UnivFwd
Class: shotgun
                                                                                   Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 776)
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Tel: 516 367 8884
Fax: 516 367 8874
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/mol_type="genomic DNA"
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100.0%; Pred. No. 2.5e-157;
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Plate: hs82 row: h column:
Seq primer: -21M13UnivFwd
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Contact: W. Richard McCombie
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Unpublished (2002)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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Location/Qualifiers
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/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, .b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a. "
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Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutg
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Lai,J., Dey,N., Kim,C.S., Bharti,A.K., Rudd,S., Mayer,K.F.,
Larkins,B., Becraft,P. and Messing,J.
Characterization of the maize endosperm transcriptome and it
comparison to the rice genome
Genome Res. 14 (10), 1932-1937 (2004)
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
Waksman Institute, Rutgers University
                                                                                                                                                                               CC357906 920
PUHHU36TD ZM 0.6_1.0 KB Zea
genomic survey sequence.
CC357906
CC357906.1 GI:30827306
                                1 (bases 1 to 920)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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     Genomics Consortium
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                                                                                                                                                                                                                                                                                                                                                              989
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/mol_type="mRNA"
/cultivar="W22"
/db_xref="taxon:4577"
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BZ375835
BZ375835.1 GI:25463827
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Other_GSSs: PUHHU36TB
Contact: Cathy Whitelaw
                                                     1 (bases 1 to 600)
Rabinowicz, P. D., O'Shaughnessy, A.L., Balija, V., Dedhia, N.,
Rabinowicz, P. D., O'Shaughnessy, A.L., Balija, V., Dedhia, N.,
Ratzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L.,
Zutavern, T., McCombie, W.R. and Martienssen, R.A.
Zutavern, T., McCombie, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidaae; Andropogoneae; Zea
                            Unpublished (2002)
Contact: W. Richard McCombie
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Annenberg Hazen Genome Sequencing Spring Harbor Laboratory
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  Lita Annenberg Hazen Genome Sequencing Center
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Local Similarity
Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Katzenburger,F., King,L., Miller,B., Muller,S., Zutavern,T., McCombie,W.R. and Martienssen,R.A. Genomic shotgun sequences from Zea mays (methyl-Unpublished (2002)
Contact: W. Richard McCombie
                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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ie78f08.bl WGS-ZmaysF (DH5a methyl
ie78f08 5', genomic survey sequence
BZ373363
BZ373363.1 GI:25458862
GSS.
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Plate: ie62 row: b colu
Seq primer: -21M13UnivRev
Class: shotgun
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Tel: 516 367 8884
Fax: 516 367 8874
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/cultivar="B73"
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VERSION
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Best Local Similarity
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PO Box 100, Cold Spring Ha
Tel: 516 367 88874
Fax: 516 367 8874
Email: mccombie@cshl.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
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genomic survey sequence.
CC025412
CC025412.1 GI:29440269
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Seg primer: -21M13UnivFwd
Class: shotgun
            Walbot, V.
Maize genomic sequences found using Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
                                                                                                                 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidaae; Andropogoneae; Zea.
                                                                                                                                                                                                        GSS.
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Stanford University
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAACCCACTGTACGAATAGCATCTACTGCTGTTCT 686
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                                                                                                                                                                                                                                                                                                                                                                                        AAACCCACTGTACGAATAGCATCTACTGCTGTTCT 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop: 622.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="WGS-ZmaysF (DH5a methyl filtered)"
/clone lib="WGS-ZmaysF (DH5a methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleoTide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector (:x/y
reads in M13mp19, .b/g reads in pUC19). The same ligation
was transformed into DH5a."
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/db_xref="taxon:4577"
/clone="ie78f08"
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Pred. No. 1.2e-140;
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RescueMu Grid P Zea mays
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RESULT 13
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Matches
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                                                                                                                                      Zea mays
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: transposon-tagged.
Location/Qualifiers
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Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                     BZ359336 1 GI:25059030 646 bp DNA linear Gi id72d02.bl wGS-ZmaysF (JM107 adapted methyl filtered) genomic clone id72d02 5', genomic survey sequence.
BZ359336 BZ359336.1 GI:25059030
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                                                                                                                                                                                     GSS.
1 (bases 1 to 646)
Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V.,
Katzenburger, F., King, L., Miller, B., Muller, S.,
                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCATTATGCGGCATAGGTGTTACATCGCGTATACAACTTAACCGTACACCACTTTTAGCA
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/clone lib="3591 - RescueMu Grid P"
/note="Organ: leaf; Vector: RescueMu (engineered from
/pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
/RescueMu is a 4.9 kb, modified maize Mu transposon
/designed to allow plasmid rescue from total genomic DNA.
/Mu elements insert preferentially into transcription
/nu elements insert preferentially into transcription
/nuits. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
/RescueMu.' Grid P was grown at Molokai in 2002. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
and BglII, and ligated to form circular plasmids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ampicillin."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic_DNA"
/cultivar="mixed_background_W23/A188/B73/K55"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
/lab_host="DH10B"
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Nascimento, L.,
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Plate: id72 row: d column: 02
Seq primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 646.
Location/Qualifiers
                                                                                Zea mays
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lita Annenberg Hazen Genome Seque Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor,
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Contact: W. Richard McCombie
                                                                                                                                               BE372017 650 bp DNA 1: ie62b08.b1 WGS-ZmaysF (DH5a methyl filtered) ie62b08 5', genomic survey sequence.
BZ372017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 516 367 8884
Fax: 516 367 8874
                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleoTide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, .b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a. "
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/cultivar="B73"
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                    to 650)
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100.0%; Pr
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O'Shaughnessy, A.L., Balija, V., Dedhia, N.,
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Pred. No. 4.2e-130;
0; Mismatches 0;
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                                                                                 BZ363755 428 bp DNA linear Gid90d01.g1 WGS-ZmaysF (JM107 adapted methyl filtered) genomic clone id90d01 5', genomic survey sequence.
BZ363755
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Plate: ie62 row: b colu
Seq primer: -21M13UnivFwd
Class: shotgun
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Contact: W. Richard McCombie
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Location/Qualifiers
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/note="Organ: immature ears; Site 1: Xba I; Itt 2: Xba I;
The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mpl9, .b/g reads in pUCl9). The same ligation
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clone="ie62b08"
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/cultivar="B73"
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                                                                GI:25068831
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Pred. No. 1.9e-128;
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1 (bases 1 to 428)

Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zutavern, T., McCombie, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
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Plate: id90 row: d column:
Seg primer: -21M13UnivRev
Class: shotgun
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Location/Qualifiers
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                              TAACTTCTGCTCGTTGCAAACCCACTGTACGAATAGCATCTACTGCTGTTCT 686
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                                                                                        CACCACTTTAGCAATGGCTCGTAATGCGGCATCTCTTCCGCTACCAGCACCTTTACCA
                                                                                                                                                                                     TAGGAGGTCGACATCCATTATGCGGCATAGGCGTTACATCGCGTATACAACCTTAACCGTA 180
                                                                                                                                                                                                                                                                               /clone lib="WGS-ZmaysF" (JM107 adapted methyl filtered)"
/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in M13mp19, .b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a. "
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/mol_type="genomic DNA"
/cultivar="B73"
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clone="id90d01"
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99.7%;
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Pred. No. 9e-122;
0; Mismatches 1; Indels
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Search completed: February 10, Job time: 8001.05 secs 2005, 17:01:49

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

, 10	18 1	c 17 1	c 16 1	c 15 1	C 14 1	c 13 10	c 12 1	c 11 1	c 10 16		C 8 16	c 7 1	c 6 16	c 5 16	C 4 16	c 3 1	2 19	1 15	Result No. Score	
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AF111709	MLIS57546	AC118277	AF458960	AF340167	MUSPERB	CHKTRANGLU	GGU47273	HSVTKY	128938	E06014	AR038124	MUSPGER	BC058742	E06015	MUSPGERB	AF266477	AK111750	128939	AR038125	RNEP3ALPH	RATREP3	AF302686	RATPEPSR	RNEP3B	Contract on
AF111709 Oryza sac				AF34016/ Screpcomy	DI/406 Mus muscuru	L02270 Chicken tra	047273 Gaile gail	KUZIZZ Marmoset ne	T Seguence T	E06014 DNA encoun	ARUJULZ4 Sequence	D10204 Mus musculu	BC058742 Mus muscu	E06015 DNA encogin	DISSE MUS muscuru	AF2664// Canis ram	AKILI750 Oryza sac	128939 Sequence 3	AR038125 Sequence	X83855 K.norvegicu	DI4869 Raccus Horv	Arsozooo xarrus no	אמר ווינואה		

# ALIGNMENTS

RESULT 2 AX342368 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy Db	Query Match Best Local Matches 1	ORIGIN	JOURNAL FEATURES	REFERENCE AUTHORS TITLE	VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AX342370 LOCUS DEFINITION ACCESSION
AX342368 498 bp DNA 1 Sequence 7 from Patent EP1167531. AX342368 AX342368.1 GI:18151811 synthetic construct	1 TGTAGCGGCCCACGCGTGG 19	100.0%; Score 19; DB 6; Similarity 100.0%; Pred. No. 24; 9; Conservative 0; Mismatches 0;	/organism="synthetic construct" /mol type="unassigned DNA" /db_xref="taxon:32630" /note="Zea maize genomic and vector	Tor detection thereof. Patent: EP 116/531-A 9 02-JAN-2002; Monsanto Technology LLC (US) Location/Qualifiers	other sequences; arcificat sequences.  1  Behr,C.F., Hironaka,C., Heck,G.R. and You,J.  Corn transformant pv-zmgt32 (nk603) and compositions	AX342370.1 GI:18151813 synthetic construct synthetic construct	19 bp DNA from Patent EP1167531.
linear		Length 19; Indels	r DNA"		positions		linear
PAT		0,			and		PAT
12-JAN-2002		Gaps 0;			methods		12-JAN-2002

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rpoB Gene Sequencing for Identification of Corynebacterium Species
J. Clin. Microbiol. 42 (9), 3925-3931 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium afermentans subsp. lipophilum
Corynebacterium afermentans subsp. lipophilum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Monsanto Technology LLC (US)
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Corn transformant pv-zmgt32 (nk603) and compositions and methods
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/protein_id="AAS89228.1"
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DECKDKOINYSAPLYVTAEFINNDTQEIKSQTVFIGDEFLMTDGTFIVGVETRVVVS
QLVRSPGVYFDETIDKSTERPLHSVKVIPSRGAMLEFDVKRDTVGVRIDRRKRQPYT
VLLKALGWTTEQITERFGFSEIMMSTLENDGVSNTDEALLEIKKQRPGEQPTRDLAQ
SLLENSFFKAKRYDLARVGRYKTNRKLGLGGDHDGLMTLTEEDIATTLEYLVRLHAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="synthetic construct"
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/mol type="unassigned DNA"
/db_xref="rtaxon:32630"
/note="1-304 Zea maize genomic DNA 305-349 construct
vector DNA 350-498 rice actin 1 promoter DNA"
                                                                                                                                                                                                                                                           /gene="rpoB"
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|mol_type="genomic DNA"
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ipophilum"
                                                                                                                                                                                                                                                                                                                                                              clone="carpob37"
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Moulin, Marseille
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AY271325
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Novel Polymorphic Region of the rpoB Gene Containing Mycobacterium
Species-Specific Sequences and Its Use in Identification of
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                    Submitted (03-APR-2003) Biomedical Laboratory Science, College
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ANSKPNRDGDVMVDGEGKTTLFDGRSGEPYKYPISVGYMYMLKLHHLVDEKIHARSTG
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VIADOGGTKOGEMALGRNLLVAFMPMEGHIZDAIILMQRVVEBDILTSVHIEBHEID
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                                                                                                                                                                                                    <1. .>189
                                                                                                                                                                                                                                             /organism="Mycobacterium
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QTTMTVPGGVEVPVEVDD"
                                                                                                                                                                                                                          /note="type:
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AY271340/c
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gene, partial (
AY271897
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Lee, H., Bang, H.E., Bai, G.H. and Cho, S.N.

Lee, H., Bang, H.E., Bai, G.H. and Cho, S.N.

Novel Polymorphic Region of the rpoB Gene Containing Mycobacterium Species-Specific Sequences and Its Use in Identification of
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AY271340
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Lee,H., Bang,H.E., Bai,G.H. and Cho,S.N. Novel Polymorphic Region of the rpoB Gene Containing Mycobacterium Species-Specific Sequences and Its Use in Identification of
                                                 Mycobacterium kansasii
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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16; Conser
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                                         (bases 1 to 204)
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larity 100.0%; Pred. No. 4.
Conservative 0; Mismatches
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Bang, H.-E., Park, H.-J.,
Direct Submission
Submitted (10-APR-2003)
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J. Clin. Microbiol. 41
12734283
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Corynebacterium riegelii strain
partial cds.
AY492278
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13385, F
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Direct Submission
Submitted (01-DEC-2003) Unite des Rickettsies
Faculte de Medecine de Marseille, 27 Bd. Jean
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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16; Conser
                                                                                                                                                                                                                                                                                                                                       Khamis,A., Raoult,D. and La Scola,B. rpoB Gene Sequencing for Identification of C J. Clin. Microbiol. 42 (9); 3925-3931 (2004)
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1. .>3180
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Pred. No.
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Ri, Heungup-Myun, Wonju, Kangwon-Do 220-710,
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                                                                                     Corynebacterium riegelii"
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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rpoB Gene Sequencing for Identification of Corynebacterium Species
J. Clin. Microbiol. 42 (9), 3925-3931 (2004)
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SEMTSPSGEI I PI STDDI DHFGNRRLRTVGELLQNQVEVGLSEMERVVRERMTYQDAE
SITPTSLINVRFVSAAIREFFGTSQLSQFMDQNNSLGGITHKRRLSALFGGLSGNEGGLSRERA
GIEVRDVHPSHYGRMCP I ETPEGPNIGLIGALASYARVNPGFF I ETPYQKVNDGKLTD
QVDYLTADEBDRYA I AQAATPMDKDGNLTGER I EVRLKDGDI GVVGPKGVDYLD I SPR
QNVSVATAMI PFLEHDDANRALMGANNQKQA VPLLRAEAAYVAFGMEQRAAYDAGDTV
I SPKAGVVETVTGDY I TVMDDEGGRDTYMLRTFERTNQGTVOTP I VSQDRVEAGQ
VI ADGRGTKDGEMALGHNLLVARMPGGHNEGH I RI GADVRDGDI LVGKVTPKGETELTP
ERRLLRAI FGEKAREVRDTSLKVPHGEQGKVI AVRRFAREDDDDLAFGVNEMI RVYVA
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BVHLGMLAKAGMTVNÞDDÞKNAKLLETLÞEHLYDVÞANSLTATÞVFDGATNDEIAGLL
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LVGTSSWREBREQQLRGETARVTSGLEDIDEEISPIQDYSGNMSLGLSBERFEDVKYTI
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QLVRSPGVYFDETIDKSTERPLHSVKVIPSRGAWLEFDVDKRDTVGVRIDRKRRQPVT
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;1. .>3330
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                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                            clone="cmrpob32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to 3330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:46360979
                                                                                                                                                                                                                                              xref="taxon:57171"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.2%; Score 16; DB 1; L
100.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3330 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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CIP 105129 RpoF
                                                                                                                                                                                                                                                                                                                          mucifaciens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (rpoB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCT 14-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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KEYWORDS

ACCESSION

VERSION

FEATURES

SGS

JOURNAL

FEATURES

Sg

JOURNAL

PUBMED

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JOURNAL
PUBMED
REFERENCE
AUTHORS
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TITLE
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ORGANISM
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AY492259/c
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VERSION
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Best Local
                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               885 TGTÁGCGGCCCÁCGCG 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-DEC-2003) Unite des Rickettsies CNRS UMR6020 IFR48, Faculte de Medecine de Marseille, 27 Bd. Jean Moulin, Marseille
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium imitans
Corynebacterium imitans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium imitans strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               La Scola, B., Khamis, A. and Raoult, D. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AY492259.1 GI:46360975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AY492259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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VRDVHPSHYGRMCPIETPEGRNIGLIGALASYARVNPFGFIETPYQKVDDGKLTDQID
YLTADEBRYAIAQAATPMDKDGNLTGERIEVRLKDGDIGVVGPGGVDYLDISPRQNV
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DGPGTKDGEMALGRNLLVAFMPWEGHNYEDAIILNQRVVEEDILTSVHIEEHEIDARD
TKLGAESITREIPNVSEDVLKDLDERGIIRIGADGOILVKAVTPKGELFLFPEER
LLRAIFGEKAREVRDTSLKVPHGEQGKVIAVRRFSREDDDDLSPGVNEMIRTVVARX
KIQDGDXMAGRHGNKGVVGKILPQEDMPFMADGTPVDIILNTHGVPRRWNIGQVLEIN
LGWLAKAGWTVNPDDPKNAKKLETLPEHLYDVPADSLTATPVPDGATNDEIAGLLANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KALGWTTEQITERFGFSEIMMSTLENDGVSNTDEALLEIYRKQRPGEQPTRDLAQSLL
ENSFFKAKRYDLARVGRYKVNRKLGLGGDHDGLMTLTEEDIATTLEYLVRLHAGETEM
TSPEGEIIPINTDDIDHFGNRRLRTVGELIQNQVRVGLSRMERVVRERMTTQDAESIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="G1:46360980"
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RSPGVYFDETIDKSTERPLHSVKVIPSRGAWLEFDVDKRDTVGVRIDRKRRQVTVLL
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                                                                                                                                                                      <1. .>3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPNRDGDVMVDENGKTTLFDGRSGEPYKYPISVGYMYMLKLHHLVDEKIHARSTGPYS
                                                                                                                                                                                       /gene="rpoB"
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                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                    db_xref="taxon:156978"
                                                                                                                                                                                                                                                                                                                                                                                  .3333
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100.0%; Pr
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105130 RpoB (rpoB)
                                                                                                                                                                                                                                                                                                                                                          imitans"
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RESULT 10
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGTAGCGGCCCACGCG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               La Scola,B., Khamis,A. and Raoult,D.
Direct Submission
Submitted (01-DEC-2003) Unite des Rickettsies CNRS UMR6020 IFR48,
Faculte de Medecine de Marseille, 27 Bd. Jean Moulin, Marseille
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Khamis,A., Raoult,D. and La Scola,B. rpoB Gene Sequencing for Identification of Corynebacterium Species J. Clin. Microbiol. 42 (9), 3925-3931 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium auris
Corynebacterium auris
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AY492234.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15364970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 3357)
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KDDINYSAPLYVTAERINDTOEIKSQTYFIGDFPLMTDKGTFEIVNGTERVVVSQLV
RSGVYFDETIDKSTERPLHAVKVIPSGAMLEFDVDKRDTVGVRIDRKRRQFVTVLL
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PTSLINVRPVSAAIREFFGTSQLSQPMDONNSLSGLTHKRRLSALGPGGLISERAGVIB
VADVHSSHYGRNCPIETPEGPNIGLIGALSSYARVNPFGFIETPYRKVDNGQLTDQID
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SVATAMIPFLEHDDANRALMGANMHKQAVAPLLARAFVVATGMEGRAYDAGDTVISP
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LGMLAKAGMTVNEDDPANAALLETLPEEMPFMEDGTPVDIILNTHGVPRRMNIGQVLEVH
LGMLAKAGMTVNEDDPANAALLETLPEEKLYDVPPESLTATPVPFDGASNDEIAGLLANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          France
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                                                                                                                                                                                                                              gene="rpoB"
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                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:44750"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Corynebacterium auris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:46360925
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Pred. No.
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ches 0;
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gene, partial
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VERSION KEYWORDS

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DEFINITION

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SOURCE

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Matches

REFERENCE AUTHORS TITLE JOURNAL PUBMED REFERENCE AUTHORS

REFERENCE AUTHORS TITLE

JOURNAL

FEATURES

gene Sg

REFERENCE AUTHORS TITLE

JOURNAL PUBMED

TITLE JOURNAL

FEATURES

Sg gene

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Nocardiaceae; Rhodococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           La Scola, B., Khamis, A. and Raoult, D. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhodococcus equi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L5364970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTAGCGGCCCACGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 3357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 3357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSPGVYFDETIDKSTERPLHSYKVIPSRGAMLEFDVDKRDTVGVRIDKKRQPVTVLL
KALGWTAEQITERFGFSEIMMSTLESDGVANTDEALLEIYRKGRPGEOFTRDLAQSLL
ENAFFRAKRYDLARVGKYKVNRKLGLGGDHDGLMTLTEEDIATTLEYLVRLHAGETEM
TSPNGAVVRINTDDIDHFGNRRLRTVGELIONQVRVGLSKMERVVRERWTTQDAESIT
TSPNGAVVRINTDDIDHFGNRRLRTVGELIONQVRVGLSKMERVVRERWTTQDAESIT
PTSLINVRPVSAAIREFFGTSQLSQFMDQNNSLSGLTHKRRLSALGPGGLSRERAGIE
VRDVHPSHYGRNCFIEFFEGPNIGLIGALASYARVNAFGFIETFYQKVEDGRLTDQID
YLITADEEDRYAIAQAATPMNAERELIAERIEVRLKOGDIGVVGPGGVDYLDIS BROMV
SVATAMIFFLEHDDARRALMGAMMQKQAVPLLRSEAPYVATGMEQRAAYDAGDTVITR
KSGAVNNVTGOPITTNDDEGIODTYMLATFERFNQGTCYNQVFIVSQGERVEAGQVIA
DGPGTKNGEMSLGRNLLVAFMPWEGHNYEDAIILNQRVVEEDILTSVHIEEBEIDARD
TKLGAEEITREIFNVSEDVLKULDERGIIRIGADVRDGDILVGKVTPKGETELTPEER
LLRAIFGEKAREVRDTSLKVPHGETGKVIAVRERFSREDDDLMPGVNEMIRVYVAQKR
KIQDGKNAGRHGNKGVVGKIIPQEDMFPMEDGTPVDIILNTHGVPRRMNIGQVLEVH
LGWLAKAGWTVNPDDDANAELLETLPEHELYDVPAESLTATFVPFDGATNEEIAGLANT
KPNRDGDVMVNGDGKARLFDGRSGEPFKYPVSVGYMYMLKLHHLVDEK.HARSTGPYS
MLTQQPLGGKAQDGGGRGEMEVMAMQAYGAAYTLQELLTIKSDDVVGRVKVYEAIVK
GINTENGSTERSERVITITETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               France
                                                                                                                                                                                                                                                                                                                                                                    /note="conspecificity: Corynebacterium equi (type CIP 54.72) = Corynebacterium hoagii (type strain C 81.17); type strain of Corynebacterium hoagii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDNIPDPGIPESFKVLLKELQSLCLNVEVL"
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PGVYFDESIDKSTEKTLHSVKVIPGRGAWLEFDVDKKDTVGVRIDRKRRQPVTTLLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .3357
                                                                                                                                                                                                                                                                                    /gene="rpoB"
<1. .>3357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
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                                                                                                                                                                                                                                                       gene="rpoB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="rerpob56"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Rhodococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:46361027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIP 81.17 RpoB (rpoB) gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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VERSION KEYWORDS

DEFINITION ACCESSION

SOURCE

ORGANISM

밁 S ORIGIN

Matches

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KEYWORDS
SOURCE
ORGANISM
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ACCESSION
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Direct Submission
Submitted (26-MAR-2003) Unite des Rickettsies, Faculte de Medecine,
Submitted (26-MAR-2003) Unite des Rickettsies, France
27 Boulevard Jean Moulin, Marseille 13385, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3702 bp 1
Mycobacterium wolinskyi strain ATCC
AY262743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium wolinskyi
Mycobacterium wolinskyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rapidly growing mycobacteria
J. Clin. Microbiol. 41 (12), 5699-5708 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adekambi, T., Colson, P. and Drancourt, M. rpoB-based identification of nonpigmented and late-pigmenting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AY262743.1 GI:34595758
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Adekambi,T.D., Dranc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14662964
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PPTKESAQTLLENLFFKERKYDLABVGRYKVKLGLANGKPTTSSTLTEEDVARTIE
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VATAMI PFLIEHDDANRALMGANNGQAVPLVRSEB-LVGTGMELRAAVDAGDV VTEK
TGVVEEVSSDYVTVMADDGSRTTYRLRKFARSNGGTCANORPI VDEGGRVEAGQVLAD
GPCTENGEMALGKNILVAIMPMEGHNVEDAII LSQRIVEEDVLITS IHLEEHEI DARDT
KLGABEI TRD I PNVSDEVLADDLERGI VR I GAEVNDLVGKVTPKGETELT PEBRL
LRAI FGEKAREVRDTSLKVPHGESGKVI GIR VFSREDDDDLPFOVNELVRVYNAXRA
LRAI FGEKAREVRDTSLKVPHGESGKVI GIR VFSREDDDDLPFOVNELVRVYNAXRA
LRAI FGEKAREVRDTSLKVPHGESGKVI GIR VFSREDDDDLFPOVNELVRVYNAXRA
LODGDKLAGHHGNKGVI GKIL PQEDMPFLPDGTPVDI I LNTHOVPRRMNI GGVLETHL
TODGDKLAGHHGNKGVI GKIL PQEDMPFLPDGTPVDI I LNTHOVPRRMNI GGVLETHL
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LFFKDKRYDLARVGRYKINKKLGINTGLDIEGITEDDIVTTELDVIKLHAGDTWMT
AFGGVEVPVEVDDIDHFGNRRLRTVGELIQNGIRVGLSRMERVVRERMTTQDVEAITE
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RDVHPSHYGRMCPIETPEGPNIGLIGSLSVYARVNPFGFIETPYRKVENGQLTDQVDY
YLVRLHEGQTTMTVPGGVEVPVEVDDIDHFGNRRLRTVGELIQNQIRVGLSRMERVVR
ERMTTQDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALG
PGGLSRERAGLEVRDVHPSHYGRMCPIETPEGPNIGLIGSLSVYARVNPFGFIETPYR
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LPNRDGERMVGPDGKATLFDGRSGEPFPYPVSVGYMYIIKLHHLVDDKIHARSTGPYS
MITQQPLGGKAQFGGQRFGEWECWAMQAYGAAYTLQELLTIKSDDVVGRVKVYEAIVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
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/db_xref="ATCC:700010"
                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mycobacterium wolinskyi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     xref="taxon:59750"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.2%; Score 16; DB
100.0%; Pred. No. 1.6
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "type strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Mycobacterium wolinskyi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.6e+02;
hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
C 700010
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RpoB gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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a, complete cds.
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PUBMED REFERENCE AUTHORS TITLE

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FEATURES

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RESULT 12

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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
AY147167/c
LOCUS
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Matches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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Mycobacterium septicum strain ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boulevard Jean Moulin, Marseille 13285, France Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (03-SEP-2002) Unite des Rickettsies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete cds.
AY147167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adekambi,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fortuitum complex by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adekambi, T., Drancourt, M. and Raoult, D. Taxonomy and identification of Mycobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium septicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 3868)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMQRQAVPLVRSEAPLVGTGMELR
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RELVRYVVAQKEKISDGDKLAGRHGNKGVIGKILPVEDMPFLPGTPVDIILWTHGVP
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EGELAGLLGSTLPNRDGEVMVNADGKATLFDGRAGEPFYPVTVGYMYLIKLHHLUDD
KIHARSTGPYSMITQQPLGGKAQFGGORFGEMECWAMQAYGAAYTLQELLTIKSDDTV
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MVRRKGGEVENVAPSDVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMQRQAVP
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PDEALLDIYRKLRFGEPFTKESAQTLLENLFFKEKTVDLARVGXXKVNKKLGLNAGQP
ITSGTLTEBDVATIEYLVRLHEGGYTMTVPGGVEVPVEVDDIDHFGNRRLRTVGELI
QNQIRVGLSRMERVVRERMTTQDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQN
                                                                                                                                                           RVSFAKLREPLEVPGLLDVQTDSFDWLVGADGWRQKAVDRGETNPKGGLEEVLEELSP
IEDFSGSMSLSFSDPRFDEVKAPVDECKDKDMTYAAPLFVTAEFINNNTGEIKSQTVF
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/trans1ation="MAANGPAYQLSGKSHEVLEGCILAVSSQSTANANTUNSVPGAPN
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118. .3675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERAAANLGINLSRNESASVEDLA"
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118. .3675
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/db_xref="ATCC:700731T"
                                                                                                                                                                                                                                                                                                                                                                       gene="rpoB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mycobacterium septicum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .3868
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Mycobacteria
te sequencing of
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. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA linear BCT 01-SEP-2003
700731T RpoB (rpoB) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from Mycobacterium the rpoB gene
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AIILSNRLVEBDVLTSIHIEEHEIDARDTKLGAEEITRDIPNVSDEVLÄDLDERGIVR
IGAEVRDGDILVGKVTPKGETELTPEREKLERAIFGEKAREVRDTSLKVPHGESGKVIG
IRVFSREDDDELPAGVNELVRVYVAGVRKISODEKLAGHEIGNKGVIGKILFVERMPFM
PDGTPVDIILWTHGVPRAKNIGQILETHLGWVAKAGWNIDVAEGTPEWASRLPDGLHS
APVDSIVSTPVPDGAREBELAGLLGSTLPNRDGDVMVNAADKATLFDGRSGEPFPYPV
TVGYMYILKLHHLVDDKIHARSTGPYSMITQQPLGGKAGPFGGMEGCMMQAYGA
AYTLGELLTIKSDDTVGRVKYYEAIVKGENIPEFGIPESFKVLLKELQSLCLNVEVLS
SDGAAIEMRDGDDEDLERAAANLGINLSRNESASVEDLA"

Matches Best Query Match

16;

Conservative

0

Local

Similarity

84.2%;

Score 16; Pred. No. Mismatches

DB 1; L 1.6e+02; 0

Length 3906; Indels

0

Gaps

0

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JOURNAL
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AUTHORS
TITLE
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AY147173/c
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KEYWORDS
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
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Mycobacterium fortuitum strain A
complete cds.
AY147173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-SEP-2002) Unite des Rickettsies, Faculte de Medecine,
Boulevard Jean Moulin, Marseille 13285, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adekambi,T., Drancourt,M. and Raoult,D. Taxonomy and identification of Mycobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taxonomy and identification of Mycobacteria fortuitum complex by complete sequencing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adekambi, T., Drancourt, M. and Raoult, D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 3906)
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EDVVATIETIVELHEGQTTMTVPGGVEVPVEVDDMDHFGNRELETVGELIQNQIRGE
EDVVATIETIVELHEGQTTMTVPGGVEVPVEVDDMDHFGNRELETVGELIQNQIRVGL
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KRELSALGFGGLSRERAGLEVEDVHSSHYGRMCPIETPEGPNIGLIGSLSVYARVNF
GFIETPYRKVVDGVVTDQIDYLTADEEDRHVVAQANSPIDEDGRFTEDRVMVRRKGGE
VENVAPSDVDYMDVSPRQMVSVATAMIEFLEHDDANRALMGANVGQAVVEVRSSAPL
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                                                                                                                                                                                                                                                                                                                                                                                            'gene="rpoB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xref="taxon:1766"
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Pred. No.
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49403T RpoB (rpoB) gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from Mycobacterium the rpoB gene
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ILNTHGVPRRMNIGQILETHLGWVAKAGWNIDVAAGTPEWASKLPEQLYSAPVDSIVS
TPVFDGAREEELAGLLGSTLPNRDGDVMVNADGKATLFDGRSGEPFPYPVTVGYMYIL
KLHHLVDDKIHARSTGPYSMITQQPLGGKAQFGGQRFGEMECWAMQAYGAAYTLQELL
TIKSDDTVGRVKVYEAIVXGENIPEFGIPESFKVLLKELQSLCLNVEVLSSDGAAIEM
RDGDDEDLERAAANLGINLSRNESASVEDLA"
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AUTHORS
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SOURCE
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Mycobacterium goodii strain ATCC 700504 RpoB gene, complete cds.
AY262736
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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27 Boulevard Jean Moulin, Marseill
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J. Clin. Microbiol. 41 (12),
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                                                                                    / WASTE STATES AND AND ASSESSMENT TONIS VPGAPURUS FAKIREPLE VPGI 
/ LTAINEL BLT 101 - WILEGCILAVSSOSKSINA TINNS VPGAPURUS FAKIREPLE VPGI 
LDVQTDS FEWILVGS DRWRQAAI DRGEEN PVGGLE VILAELS PIEDFSGSMSLS FSDPR 
PDEVKAS VDECKOKOMTY AAP LFVTAEF INNITGE I KSQTVENGD P PMMTEKGTFI IN 
GTER VVVSQLVRS PGVY FDETI DKSTEKTILS VKVI PIGRGAMLE BYDVKRDTYGVRI DI 
RKRQP VTVLLKALGWTNEQ I VERFGGSE I MMGTLEKDTTSGTDEALLD I YRKLRPGE 
PPTKESAQTILLENLF FKEKRYDLARVGRYKVKKLGLINAGKPI TSSTLTEED VVATIE 
YLVRLHBGQTTMTV PGGVEV PVEVDD I DHPGUREL TRYGELI QNQ I RVGLSRMER VVR 
YRUTHLBGQTTMTV PGGVEV PVEVDD I DHPGUREL RFTGELI QNQ I RVGLSRMER VVR 
YRUTHLBGQTTMTV PGGVEV PVEVDD I DHPGUREL RFTGLE (WVRKKGGEVE FVSAQ 
VDYMDVS PRQMVS VATAMI PFLEHDDANAS FTDENGR FTEER (WVRKKGGEVE FVSAQ 
VDYMDVS PRQMVS VATAMI PFLEHDDANAS FTDENGR FTEER (WVRKKGGEVE FVSAQ 
VDYMDVS PRQMVS VATAMI PFLEHDDANAS HAMDANNORQA VPLVRSEAPL VCTGMELR 
AAIDAGDVVJADATGV LEEVSADY I TVMADDGTRQS YELRKFARSHHGTCANQR PI VD 
AGQRUBAGQVI ADGPCTQNGEMALGKNLLVALMPWEGHNYEDAI I LSARLVEEDVLTS 
IHI EEHHI DARDTKLGABEI TRD I PNVS DEVLADLDERGI VR I GABEVRDDDELPAGV 
NELVR VYVAQKRKI SDGDKLAGRHGNKGVIGKI LFVEDMPFLPDGTPVDI I LNTHGVP 
RRMNI GQILETPELGWAKAGGWI DVAAGV PDWASKLPEELYTA PSDS I VAT PVFDGAQ 
RCCH ACH I GGRT, MDROCS FWANANA OCCA ATT FORDS GETOED DVS TOW THE TAIL INTIN 
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/mol_type="genomic DNA"
/strain="ATCC 700504"
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/protein_id="AAQ76595.1"
/db_xref="GI:34595745"
GRVKVYEA I VKGEN I PEPGI PESFKVLLKELQSLCLNVEVLSSDGAA I EMRDGDDEDL
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/db_xref="taxon:134601"
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ADS56566 ABX42572 ACH29799	ACF04818 ADL13471 ACD72269 ABX54979	AAQ46125 ABV75862 AAQ46124 ABV75863	ADM43175 ADM43175 ADS00140 AAI59900 AD030319 ADD72493 ADB52577	ID ABK15246 ABK15244 ABK15244	SUMMARIES
Ads56566 Bacterial Abx42572 Bovine ES Ach29799 Human tes	Act04818 Meirthlaz Adl13471 Osteoarth Acd72269 E. coli K Abx54979 Bovine ES	Aag46125 PGE2 rece Abv75862 Human pot Aag46124 PGE2 rece Abv75863 Human pot	Admillary Wild-type Admillary Wild-type Adsollary Wild-type Aais9900 Human pol Ado30319 Mouse GPC Adp72493 Renal tox Adb52577 Primary r	Description Abk15246 Corn tran Abk15244 Corn nk60 Abk15244 Corn nk60	

The invention relates to a DNA construct (I) comprising a first (F1) and a second (F2) expression cassette. F1 of the DNA construct, in operable

Claim 8; Page 3; 25pp; English

Novel DNA construct useful for producing a corn plant that tolerates application of glyphosate herbicide, comprises two transgene expression

WPI; 2002-165871/22.

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Hironaka C,

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RESULT 1 ABK15246 ID ABK15246		C 45		<u>.</u>	C 42	4		w	w	c 37	w	w	w	w	ω	w	; س	Ŋ.	28	27	N	c 25	N	N	22	c 21	
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standard; DNA; 19		73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	
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Probe; 88; rice actin 1 promoter; RA1; RA1 intron; chloroplast transit peptide gene; glyphosate resistance; corn; 5-enol-pyruvylshikimate-3-phosphate synthase; EPSPS; Hsp70 intron; transcriptional terminator; cauliflower mosaic virus 35S promoter; PV-ZMGT32; transgenic; nk603.
                                                                                                                                                                                                                             Zea mays.
Synthetic.
                                                                                                                                                                                                                                                                                                             Corn transgene junction probe #1
                                                                                                                                   22-JUN-2000; 2000US-0213567P.
13-OCT-2000; 2000US-0240014P.
13-OCT-2000; 2000US-0241215P.
                                                                                                                                                                                           02-JAN-2002.
                                                                                                                                                                                                            EP1167531-A1.
                                                                                                                                                                                                                                                                                                                                  08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                   ABK15246;
                                                                                                                                                                         15-JUN-2001; 2001EP-00202314
                                                                                                                   (MONS ) MONSANTO TECHNOLOGY LLC.
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RESULT 2
ABK15244
ID ABKJ
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Best Local S
Matches 19
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                                                                                                                                                       22-JUN-2000;
13-OCT-2000;
13-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chloroplast transit peptide gene; glyphosate resistance; corn; 5-enol-pyruvylshikimate-3-phosphate synthase; EPSPS; Hsp70 int transcriptional terminator; cauliflower mosaic virus 35S promo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa.
Synthetic.
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Novel DNA construct useful for producing a corn plant that tolerates
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                                                                                                                                                                                                                                                                                                              EP1167531-A1
                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                                           Hironaka C,
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2000US-0240014P.
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Pred. No. 0.14;
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                                                                                                                                Sequence 498
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         application of glyphosate herbicide, comprises two transgene expression
                                                                                                                                                                   sequences
296
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                                                               19;
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                                                                                  Similarity
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                      TGTAGCGGCCCACGCGTGG
TGTAGCGGCCCACGCGTGG
                                                                  Conservative
                                                                                                                                  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                  148 A; 114 C; 131 G;
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                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
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314
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                                                                                 Score 19; D
Pred. No. 0.
                                                                  Mismatches
                                                                                                                                  105 T; 0 U; 0 Other;
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                                                                                  .097;
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                                                                                                Length 498
                                                                  Indels
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                                                                  Сарв
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RESULT 3
AAS05219/c
ID AAS05219
Lee
                                                                                                                                                     Mycobacterium
                                                                                                        27-OCT-1999;
                                                                                                                    27-OCT-2000;
                                                                                                                               03-MAY-2001.
                                                                                                                                          WO200131061-A1
                                                                                                                                                               Non-tuberculous mycobacteria; rpoB gene fragment; NTM; PCR-restriction fragment length polymorphism analysis;
                                                                                                                                                                                 Mycobacterium
                                                                                                                                                                                            07-SEP-2001
                                                                                                                                                                                                       AAS05219;
                                                                                              (ERUM-)
                                                                                  ŗ
                                                                                  Park YK,
                                                                                              ERUME
                                                                                                                                                                                                                  standard; DNA;
                                                                                                                    2000WO-KR001223
                                                                                                                                                                                            (first
                                                                                             BIOTECH CO
                                                                                                                                                                                fortuitum rpoB gene fragment
                                                                                                                                                     fortuitum
                                                                                                        99KR-00046795
                                                                                  Bai
                                                                                                                                                                                            entry.
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                                                                                              LTD.
                                                                                   Ki:a
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                                                                                   Kia
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                                                                                   Park
                                                                                   품
                                                                                                                                                                 gb
                                                                                                                                                                      HIV; PRA; RFLP;
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WPI;

2001-300520/31.

New DNA fragments from the diagnosis and identification

rpoB on of

gene many

of mycobacteria, useful mycobacterial species b

γď

restriction

for

and identification ength polymorphism.

Claim 1;

Page

46;

50pp; English.

of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacteri species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method. The method comprisobtaining a restriction fragment length polymorphism (RFLP) pattern of The present sequence for Mycobacterium fortuitum rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial

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RESULT 4
ADM43175/c
ID ADM431
XX ADM431
XX ADM431
XX Wild-t-
XX Wild-t-
XX replic
XX replic
XX wolden
XX Genomme
CC defect
CC defect
CC comprise
CC defect
CC replic
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragments. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 pCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for detecting specific Mycobacterial species
                                                                                                                                                                                                                                                                             Bett AJ, u
                                                                                                                                                                                                                                                                                                                                                                   22-AUG-2002;
17-MAR-2003;
17-MAR-2003;
28-MAR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004018627-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unidentified adenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adenovirus serotype 24; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replication-defective adenovirus; anti-HIV; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wild-type adenovirus serotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADM43175
                                                                                                                                                                               Propagating replication-defective adenovirus in an adenoviral complementing cell line, useful in gene therapy applications, providing all or a portion of an E4 region in cis within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-AUG-2003; 2003WO-US026145
                                                                                                                                                                                                                                                                                                                                    (MERI ) MERCK & CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTAGCGGCCCACGCG
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                                                                                                                                                                                                                                                                                    Chastain:
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; 2003US-0455234P.
; 2003US-0455312P.
; 2003US-0458825P.
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                                                                                                                                                                                                                                                                                                     Σ,
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 nucleotide sequence SEQ ID NO:
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                                                                                                                                                                                                                                                                                                       Emini
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6.1;
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                                                                                                                                                                                                        comprises
                                                                                                                                                                                                                        E1-
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The present invention describes a method for propagating a replication-defective adenovirus in an adenoviral E1-complementing cell line expressing E1 gene product(s) which are non-native to the adenovirus, comprising providing all or a portion of an E4 region in cis within the genome of the replication-defective adenovirus. Also described: (1) a replication-defective adenovirus. Also described in of a replication-defective adenovirus adenovirus and or a portion of a heterologous E4 region comprising a heterologous adenoviral ORF6, or the

or that

the

Disclosure;

SEQ ID

NO 1; 133pp; English

The invention relates to a novel recombinant adenoviral vector of serotype 24 which is partially deleted in E1 and devoid of E1 activity and comprises a heterologous nucleic acid or an human immunodeficiency virus (HIV)-1 gene. A vector of the invention has anti-HIV activity, an may have a use in gene therapy, and as a vaccine. The recombinant

providing all c the adenovirus.

SEQ

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g

<u>ა.</u>

113pp;

English.

genome

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RESULT 5
ADS00140/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        covertor of serotype 24 which comprises an B4 gene or a segment of an B4 cells comprising ORF6 of an alternative serotype; (3) a population of cells comprising the recombinant adenoviral vector; (4) producing crecombinant, replication-defective adenovirus particles; (5) a purified recombinant, replication-defective adenovirus particles harvested in cercombinant adenovirus particles; (7) a prification comprising purified recombinant adenovirus particles; (7) a composition comprising purified cexpression of heterologous nucleic acid; and (8) generating a cellular-mediated immune response against HIV in an individual. The replication-defective adenovirus in an adenoviral E1-complementing cell line useful for propagating and rescuing multiple serotypes of replication-defective adenovirus in an adenoviral E1-complementing cell line useful for generating a cellular-mediated immune response against HIV in an individual. The resultant virus can be studied and used in cell line and for generating a cellular-mediated immune response against HIV in an individual. The resultant virus can be studied and used in cell various gene therapy and vaccine efforts. The present sequence represents a wild-type adenovirus serotype 24 nucleotide sequence, which is used in the exemplification of the present invention.
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Best L
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                                                                                                                                                                                                                Emini EA,
Morsy MA;
                                                                                                                         New recombinant adenoviral vector of serotype 24 which is partially deleted in E1 and devoid of E1 activity, useful for delivering and expressing exogenous genes, e.g. in gene therapy or in vaccination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 35167 BP; 7977 A; 9958 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is propagated by the method
                                                                                                                                                                                    WPI; 2004-691052/67.
                                                                                                                                                                                                                                                                                      17-MAR-2003; 2003US-0455312P
                                                                                                                                                                                                                                                                                                                                                                                                     Human adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                ds; adenovirus serotype 24; anti-HIV; vector; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADS00140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADS00140 standard;
                                                                                                                                                                                                                                                                                                                21-AUG-2003; 2003WO-US026338
                                                                                                                                                                                                                                                                                                                                              30-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                         WO2004083418-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              human adenovirus
                                                                                                                                                                                                                                Shiver JW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA; 35167
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                                                                                                                                                                                                                                  Casimiro DR,
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                                                                                                                                                                                                                                  Chastain M,
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                                                                                                                                                                                                                                   Kaslow
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RESULT 6
AAI59900/c
ID AAI599
XX Human
XX Human
XX Human
XX Human
XX Human
XX Homo
XX AIZhei
AIZhei
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21-JAN-2000;
25-APR-2000;
20-JUN-2000;
19-JUL-2000;
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14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adenoviral vector of serotype 24 which is at least partially deleted in E1 and devoid of E1 activity is useful for the delivery and expression c exogenous genes. The adenoviral vectors are useful in gene therapy or in vaccination protocols. The present sequence represents the nucleic acid
                                    immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                        Novel nucleic acids and polypeptides, as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                       system, such as peripheral
                                                                                                        encoded
                                                                                                                           The invention
                                                                                                                                                                                                                                                                     P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chemokinetic;
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DB; AAM40744.
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16; Conser
                                                                                                        polypeptides
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Wang Z,
Goodrich
                                                                                                                                                                   SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for wild-type adenovirus serotype 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-00488725.

2000US-00552317.

2000US-00598042.

2000US-00620312.

2000US-00653450.

2000US-00652191.

2000US-00693036.

2000US-00693036.
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                                                                                                      relates to human nucleic acids (AAI57798-AAI61369) eptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombolytic;
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                                                                                                                                                                 NO 3889; 10078pp;
                                                                                                                                                                                                                                                                                                                             Asundi V,
Wehrman T,
1 R, Drmanac
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                       nervous
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                                                                                                                                                                                                                                                                                                                                 Chen R,
Xu C,
c RT;
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red. No. 3.4
Mismatches
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                       injuries,
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Xue
                                                                                                                                                                                                                             useful for treating disorders
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  system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arthritis;
                       peripheral neuropathy
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gχ
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Zhang
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                            Gaitanaris
Madisen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transgenic mouse; neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; blood disorder; immune disorder; bone disorder; joint disorder; metabolic disorder; mutritive disorder; cancer; kidney disorder; liver disorder; lung disorder; breast disorder; kidney disorder; uterus disorder; prostate disorder; testis disorder; skin disorder; thyroid disorder; pancreas disorder; spien disorder; thymus disorder; thyroid disorder; antiparkinsonian; antimanic; cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic; cytostatic; antiinflammatory; vasotropic; antidiarrhoeic; antide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic; dermatological; antiulcer; antithyroid; antiallergic; anorectic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         part
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                                                                                                                                                                                                                                                                                                                                                                                                                     09-SEP-2002;
09-APR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AD030319;
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                                                                                                                                                                                                                                                                                                                                                                     (PRIM-)
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15; Conserv
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Mcilwain
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2003US-0461329P.
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                                                                                                                                                                                                                                                                                                                   Bergmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
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100.0%; Pr
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Pavlova
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lova MN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy; GPCR modulator; mouse,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:1422.
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Vassilatis 1
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20;
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Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina

Claim 151; SEQ pectoris,

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1422;

English.

graease

invention

relates 日

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human 542pp;

and

mouse

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protein-coupled receptors

(GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention, methods of treating, preventing or diagnosing disease associated with GPCRs of the invention; methods of screening for

compounds useful in the treatment of GPCR-related diseases;

a transgenic

diseases

acids

WPI; 2004-460771/43.

associated with

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RESULT 8
ADP72493/
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         Mendrick
Elashoff
                                                                                                                                                 ds; toxic effect; gene expression profile; kidney tissue; differential gene expression; toxicity progression; toxicity drug screening; toxicity assay; kidney pathology; nephritis; kidney necrosis; glomerular injury; tubular injury; foral screening.
                                                                                                                                                                                                                     26-AUG-2004
                                                                                                                                                                                                                                                         ADP72493 standard; DNA; 1183
                                                                       24-NOV-2003;
                                                                                        10-JUN-2004
                                                                                                           WO2004048598-A2
                                                                                                                                                                                                   Renal toxin progression
                                                     22-NOV-2002;
                                    (GENE-) GENE
                                                                                                                                                                                                                                                                                                       526
                                                                                                                                             segmental glomerulosclerosis.
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                                                                                                                           norvegicus.
                                                                                                                                                                                                                                                                                                                        TGTAGCGGCCCACGC 15
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                     2002US-00301856
                                                                                                                                                                                                                      (first entry)
                                                                       2003WO-US037556
                                    LOGIC INC
                 Porter MW,
                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                        512
                  Johnson KR,
                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                    marker #1082.
                                                                                                                                                                                                                                                                                                                                           Mismatches
                   Castle A,
                                                                                                                                                                                                                                                                                                                                           0;
                   Higgs
                    В,
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CC mouse comprising a GPCR gene of the invention; a mouse comprising a GPCR gene of the invention; a mouse comprising a GPCR gene of the invention; a mouse comprising a GPCR gene of the invention; a mouse comprising a comprising a mutation in a different GPCR gene of the invention; and kits comprising CPC probes which hybridise to GPCR polynucleotides of the invention. The CPC gene of the invention; and kits comprising CPC probes which hybridise to GPCR polynucleotides of the invention. The CPC comprising a GPCR nucleic acid. The GPCR nucleic acids and vectors CPC diseases including neurological disorders (e.g., Alzheimer's disease, CPC diseases including neurological disorders (e.g., Alzheimer's disease, CPC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel CPC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel CPC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel CPC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel CPC (e.g., Spout or osteoporosis); metabolic or mutritis, rheumatoid CPC anthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., autoimmne disorders (e.g., autoimmne disorders (e.g., autoimmne disorders (e.g., cohesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary cuterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence acid of the five printed specification; those sequences not shown were obtained in electronic format directly from WIPO at fig. of the wipo.int/pub/published_pct_sequences.
CC thick invention relates to a method of predicting (the progression of) a compound by preparing a gene expression profile of a compound tissue or cell sample exposed to the compound and comparing the compound and comparing the compound in a tissue or cell sample exposed to the compound, where compound in a tissue or cell sample exposed to the compound, where compound in a tissue or cell sample exposed to the compound, where compound in a tissue or cell sample exposed to the compound, where compound in a tissue or cell sample exposed to the compound, where compound in a tissue or cell sample exposed to the compound, where compound in a tissue or cell sample exposed to the compound, where compound in a tissue or cell sample exposed to the compound. The genes are compound of a teast one toxic effect of a compound. The genes are useful as toxicity markers in drug screening and toxicity assays. The compound or test agent will induce various specific kidney pathologies, such as nephritis, compound or test agent will induce various specific kidney pathologies, such as nephritis, compound or test agent will induce to compound or for fect and for compound or determining the similarity compound in the similarity of a toxic response. The methods are useful for determining the similarity conficting or modelling the potential cellular pathways influenced, compound or test agent. The kit is useful for predicting or modelling the toxic response of a test compound, for that show promise as new drug targets and for screening known and newly that show promise as new drug targets and for screening known and newly that show promise as new drug targets and for screening known and newly that show promise as new drug targets and for screening known and newly that show pathologies. This sequence corresponds to a gene marker used in the compound of the invention. (Note: The sequence data for this patent did not format directly from WIPO at fift, wipo.int/pub/published_pct_sequences).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicting (the progression of) a toxic effect of a compound, for monitoring the progression of renal disease states, comprises preparing agene expression profile of a kidney tissue or cell sample exposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; SEQ ID NO 1082; 266pp; English
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88888888888888888888888888888888888888

Query Match Best Local

Similarity

78.9%; Score 15; 100.0%; Pred. No

Pred. No.

19;

Length 1098; U; 0 Other;

Indels

0

Gaps

0

BP; 208

A; 361 C; 366 G;

248 T; 0 U; 0 Other;

Sequence 1098

BP; 185 A; 342 C;

335 G; 236

T; 0 12;

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Query Match
Best Local
                                Matches
                                                                Sequence 1183
582
               1 TGTAGCGGCCCACGC
                                         Similarity
TGTAGCGGCCCACGC
                               Conservative
                                         78.9%; Score 15; 100.0%; Pred. No.
568
                15
                                 0
                                   Mismatches
                                         DB
19;
                                                  12;
                                  0
                                                 Length 1183;
                                   ٥,
                                   Gaps
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0,

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RESULT 9
ADB52577/c
 toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
                                                                                                                                                                                                   Primary rat hepatocyte toxicity modelling related
                                                           04-FEB-2002;
                                                                                04-FEB-2003; 2003WO-US003482.
                                                                                                                     WO2003065993-A2
                                                                                                                                          Rattus norvegicus
                                                                                                                                                                                                                         04-DEC-2003
                                                                                                                                                                                                                                                                  ADB52577 standard; DNA; 1253
; 2002US-0353171P.
2002US-0363534P.
2002US-037024BP.
2002US-0371134P.
2002US-0371139P.
2002US-0371139P.
2002US-03711413P.
                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                       gene
                                                                                                                                                                                    diagnostic marker;
                                                                                                                                                                                                        SEQ ID NO:3119.
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13-MAR-2002; 08-APR-2002; 10-APR-2002;

10-APR-2002; 10-APR-2002;

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RESULT 10
AAQ46125/c
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Best Local S
Matches 15
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19-APR-2002;
22-APR-2002;
08-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUL-2002;
09-JUL-2002;
04-SEP-2002;
28-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mendrick
Elashoff
                                                                                              prostaglandin E receptor; PGE; agonist; atagonist; GTP-binding protein; digestive tract; constriction; relaxation; gastric acid; intestinal juice; neurotransmitter; ss.
                                                                                                                                                                                25-MAR-2003
09-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
                                                                        Mus musculus
                                                                                                                                                     PGE2 receptor
                                                                                                                                                                                                                                                  AAQ46125 standard; cDNA; 1405 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 44; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mean values.
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                                                                                                                                                                                                                                                                                                                        614
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15; Conserv
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                                                                                                                                                                                                                                                                                                                        TGTAGCGGCCCACGC 600
                                                                                                                                                                                                                                                                                                                                              TGTAGCGGCCCACGC 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002US-0373601P.
2002US-0374139P.
2002US-0378370P.
2002US-0378652P.
2002US-0378655P.
2002US-0378655P.
2002US-0394230P.
2002US-0394230P.
2002US-0407688P.
                                                                                                                                                                                                                                                                                                                                                                           78.9%;
larity 100.0%;
Conservative (
                                                                                                                                                                                (revised)
(first ent
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP;
                                                                                                                                                       (EP3 beta) clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID NO 3119; 874pp;
                                          Location/Qualifiers
/*tag= a
/product= "PGE2_receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                213 A; 386 C; 373 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INC.
                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson
                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                        Score 15;
Pred. No.
                                                                                                                                                       MP653
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                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                          No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  281
                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 1253;
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  0 Other;
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ABV75862;
ID ABV75862;
XX ABV75862;
AC ABV75862;
XX DT O5-FEB-200
XX Transporte
XX Transporte
XX EB:
XX Homo sapie
XX Homo sapie
XX CDS
FT CDS
FT CDS
FT 3'UTR
FT XX
FT 3'UTR
FT XX
FT 3'UTR
FT XX
FT 3'UTR
FT XX
FT ADS
FT
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGE2 is known to be involved in digestive tract conscriptions. PGE2 is known to be involved in digestive tract conscriptions. The protein encoded gastric juice secretion and neurotransmitter release. The protein encoded by the gene is capable of receiving PGE and of activating GTP-binding protein. MP653 (AAQ46125) is identical to MP660 (AAQ46124) with the exception of a 89-bp deletion in the coding region of the C-terminal tail of the receptor. This deletion creates a new reading frame downstream from this junction. This results in a 30 amino acid C-terminal fragment of the receptor being replaced with a new 26-amino acid fragment in the C-terminal end of the MP653 (AAQ46125) receptor. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1405 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New prostaglandin E receptor protein and DNA encoding prostaglandin binding, agonists and antagonists etc.
                                                                                                                                                                                                                                                                                                                                                                                                                      Transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human potassium channel transporter cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Fig 4; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ichikawa A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-FEB-1992;
23-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-SEP-1993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; cDNA; 1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTAGCGGCCCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTAGCGGCCCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.9%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Narumiya
                                                                                                                                                                                                                                                                                                                                                                                                                         potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
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92JP-00064889
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                                                                                                                                                                                                               /*tag= a
375. .1667
                                                                                                                                               /product= "T
1667. .1780
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                                                                                                                                                                                               *tag=
                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 A; 415 C; 418 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                           "Transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВР
                                                                                                                                                                                                                                                                                                                                                                                                                      human; gene therapy; chromosome 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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RESULT 12
AAQ46124/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cc rine present requence is that to come gated potassium channel cransporter family, and which is expressed in the lung and in the foetal control that is related to the voltage gated potassium channel control transporter family, and which is expressed in the lung and in the foetal control that gene (see ABV75863) encoding the transporter is located on control control the foetal services and the probes, primers, in biological assays, for constructing recombinant controling the human transporter protein, for designing ribozymes, for controling the effectiveness of modulating compounds on the expression or controling the effectiveness of modulating compounds on the expression or controling the effectiveness of modulating compounds on the expression or controling the effectiveness of modulating compounds on the expression or controling and transporter gene in clinical trials or in a construct assays for qualitative changes, in human constructs to control human transporter that while not necessarily causing a disease, convertheless affects the treatment modality, as antisense constructs to control human transporter gene expression in cells, tissues and constructs to aberrant in human transporter gene expression. A gene chip comprising a construct and is useful for conducting cell-transporter mucleic acid is claimed, and is useful for conducting cell-based ansays involving the human transporter received.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated human transporter peptide useful for treating disorder characterized by absence of, in appropriate or unwanted expression of the transporter protein, and as immunogens to raise antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Fig 1; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001US-00820923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1780 BP; 352 A; 570 C; 496 G; 362 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-058533/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beasley EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE )
                                                                                   Mus musculus
                                                                                                                                               prostaglandin
                                                                                                                                                                                  PGE2 receptor
                                                                                                                                                                                                                   25-MAR-2003
09-FEB-1994
                                                                                                                                                                                                                                                                                                     AAQ46124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KETC/)
                                                                                                                  intestinal
                                                                                                                                  prostaglandin E receptor; PGE; agonist; atagonist;
digestive tract; constriction; relaxation; gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEIM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assays involving the human transporter protein
                                                                                                                                                                                                                                                                                                                                                                                      51
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BEASLEY E M.
WEI M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
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DI FRANCESCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    AGCGGCCCACGCGTG 18
                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                      AGCGGCCCACGCGTG
                                                                                                                  juice; neurotransmitter; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002WO-US009743.
                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                  (EP3 alpha) clone MP660.
                                                Location/Qualifiers
'product= "PGE2_receptor"
                                                                                                                                                                                                                                                                                                     CDNA; 2107
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; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of cDNA encoding a novel human transporter
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RESULT 13
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New prostaglandin E receptor protein and DNA encoding prostaglandin binding, agonists and antagonists etc.
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23-MAR-1992;
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         potassium channel; human; gene therapy; chromosome 17;
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92JP-00064889.
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1294
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2374. .12713
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encoding the transporter are useful as probes, primers, in biological assays, for constructing recombinant vectors, host cells and transgenic animals, for expressing antigenic portions of the transporter protein, for designing ribozymes, for monitoring the effectiveness of modulating compounds on the expression or activity of the human transporter gene in clinical trials or in a treatment regimen, in diagnostic assays for qualitative changes in human transporter nucleic acid that lead to pathology, for testing an individual for a genotype that while not necessarily causing a disease, nevertheless affects the treatment modality, as antisense constructs to control human transporter gene expression in cells tiegnes and grazanisms and for can.
        expression in cells, tissues and organisms, and for gene therapy in patients containing cells that are aberrant in human transporter gene expression. A gene chip comprising a transporter nucleic acid is claimed, and is useful for conducting cell-based assays involving the human
                                                                                                                                                                                                          The present sequence is that of genomic DNA encoding a novel human transporter protein that is related to the voltage gated potassium channel transporter family, and which is expressed in the lung and foetal brain. The gene is located on chromosome 17. Nucleic acids
                                                                                                                                                                                                                                                                                                          Novel isolated human transporter peptide useful for treating disorder characterized by absence of, in appropriate or unwanted expression of transporter protein, and as immunogens to raise antibodies.
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P-PSDB; ABP55112.
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(WEIM/)
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DI FRANCESCO
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                                                                                                                                    Sequence 51855 BP; 7256
                                                                                                                                                                      The present invention provides the protein and coding sequences of a number of proteins involved in the biosynthesis of melithizaol. These as designated Mel B - Mel H and ORF 1- ORF 7. The sequences can be used in the production of melithizaol, which exhibits fungicidal activity. The present sequence is a coding sequence shown in the exemplification of the
                                                                                                                                                                                                                                                            New nucleic acid molecule termed mel genes encoding polypeptide synthase and non-ribosomal peptide synthetase that are involved in synthesis of melithiazol displaying enhanced fungicidal activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Melithiazol synthesis; polyketide synthase; fungicide; nonribosomal peptide synthetase; gene; ds.
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100.0%;
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                                                                                                               Length 51855;
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SAXAXE

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(first entry)

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Search completed: February 10, 2005, 13:44:04 Job time : 22.6391 secs
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                                                                                                                                                                                                                                                                                The invention relates to a method of determining susceptibility of an comprising identifying whether the individual has at least one colorophyte development and/or comprising identifying whether the individual has at least one colorophism in a polynucleotide encoding at least one of the protein colorophism in a polynucleotide encoding at least one of the protein colorophyte development and/or joint space constraint and/or osteophyte development and/or joint pain that is consociated with a disease, preferably osteoarthritis. The call line and colorophyte development and/or osteoarthritis. The call line and colorophyte development pain. This sequence corresponds to the polynucleotide encoding a protein listed in the specification. (Note: the polynucleotide encoding a protein listed in the specification. (Note: the polynucleotide encoding a protein listed in the specification but was obtained in electronic format directly from WIPO at figure individual to but was obtained in electronic format directly from WIPO at figure individual to but was obtained in electronic format directly from WIPO at figure individual to jublished pct_sequences).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining susceptibility of an individual to joint space narrowing, osteophyte development and/or joint pain comprises identifying whether individual has at least one polymorphism in a polynucleotide encoding
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-08-144-602B-6
US-08-144-602B-6
US-09-682-597A-5
US-09-682-597A-2
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US-09-377-466B-38
US-09-377-466B-38
US-09-377-466B-15
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ALIGNMENTS	US-09-949-016-192515 US-09-180-342-1 US-09-190-016-17231 US-08-368-803-8 US-08-368-803-9 US-08-368-803-9 US-09-949-016-163659 US-09-949-016-165157 US-09-949-016-180872 US-09-949-016-180873 US-09-949-016-205828 US-09-949-016-205828 US-09-949-016-1815 US-09-949-016-1815 US-09-949-016-1815 US-09-949-016-1815 US-09-949-016-1315 US-09-949-016-1315
	Sequence 192515, Sequence 1, Appli Sequence 8, Appli Sequence 9, Appli Sequence 16349, Sequence 163650, Sequence 163657, Sequence 180873, Sequence 20528, Sequence 4729, Appli Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 1852, App Sequence 1315, App Sequence 1315, App

# APPLICANT: MONBARTO CO APPLICANT: Honbarto Co APPLICANT: Heck, Catherine APPLICANT: Heck, Gregory APPLICANT: Heck, Gregory APPLICANT: You, Jinsong TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Det TITLE OF INVENTION: Thereof FILTE REFERENCE: 38-21(52258)B CURRENT APPLICATION NUMBER: US/09/872,051 CURRENT APPLICATION NUMBER: 60/213,567 PRIOR APPLICATION NUMBER: 60/213,567 PRIOR APPLICATION NUMBER: 60/241,215 PRIOR APPLICATION NUMBER: 60/241,215 PRIOR APPLICATION NUMBER: 60/240,014 PRIOR FILING DATE: 2000-10-13 PRIOR APPLICATION NUMBER: 50/240,014 PRIOR FILING DATE: 2000-10-13 PRIOR FILING DATE: 2000-10-13

US-09-872-051-7

Sequence 7, Application Patent No. 6825400 GENERAL INFORMATION:

US/09872051

SEQ ID NO 7 SOFTWARE: PatentIn version 3.0

US-09-872-051-7 IENGTH: 498

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Source
LOCATION: (1)..(498)
OTHER INFORMATION: 1-304 Zea maize genomic DNA
OTHER INFORMATION: 305-349 construct vector DNA
OTHER INFORMATION: 350-498 rice actin 1 promoter DNA

Ś 밁 á 밁 8 Query Match Best Local Simi Matches 498; 121 61 61 **_** Similarity GAGGTAAACAGATCAGCATCAGCGCTCGAAAGTTTCGTCAAAGGATGCGGAACTGTTTCC TCCAGGGTGAAGTATCAGAGGATTTACCGCCCATGCCTTTTATGGAGACAAGAAGGGGAG TCCAGGGTGAAGTATCAGAGGATTTACCGCCCATGCCTTTTATGGAGACAAGAAGGGGAG Conservative 100.0%; 0; Score 498; DB 4; Pred. No. 1.6e-244; Mismatches Length 498; Indels 0; 180 180 120 120 60

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121

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APPLICANT: Heck, Gregory

APPLICANT: You, Jinsong

ITILE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Detection of Invention: Thereof

ITILE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Detection of Invention in Thereof

ITILE OF INVENTION: Thereof

ITILE OF INVENTION: Thereof

ITILE OF INVENTION NUMBER: 60/213,567

ITILE OF INVENTION NUMBER: 60/213,567

ITILE OF INVENTION NUMBER: 60/241,215

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                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Monsanto Co
APPLICANT: Behr, Carl
APPLICANT: Hironaka, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: source
LOCATION: (1)..(1183)
LOCATION: (1)...(1183)
OTHER INFORMATION: 1-164 Agrobacterium tumefaciens nos 3' terminator
OTHER INFORMATION: 165-381 construct vector DNA
OTHER INFORMATION: 382-686 Zea maize plastid genes, rps11 and rpoA
OTHER INFORMATION: 687-1183 Zea maize genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
       321
                                                                                                                                              381 CGCGTGGTACCAAGCTTGATATCCCTAGGGCGGCCGCGTTAACAAGCTTACTCGAGGTCA 322
                                                                                                                                                                                                                                                                                            118;
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                                                TTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGGTAAGATTACC 425
                                                                                                                                                                                           CGCGTGGTACCAAGCTTGATATCCCTAGGGCGGCCGCGTTAACAAGCTTACTCGAGGTCA 367
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GENERAL INFORMATION:
APPLICANT: BAITY, Gerard F.
TITLE OF INVENTION: Phosphonate Metabolizing Pla
FILE REFERENCE: 38-21(15303)
CURRENT APPLICATION NUMBER: US/09/441,340
CURRENT FILING DATE: 1999-11-16
EARLIER APPLICATION NUMBER: 60/108,763
EARLIER APPLICATION NUMBER: 60/108,763
LABLIER FILING DATE: 1998-11-17
NUMBER OF SEO ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: terminator
; LOCATION: (2114)..(2369)
US-09-441-340-27
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US-09-441-340-27
                                                                                                                                                                                                                                                                                                                     RESULT 4
US-08-144-602B-7
                                                                                                                                                                                                                                                                           Sequence 7, Application Patent No. 5641876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 27
LENGTH: 2378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                        APPLICANT: MCElroy, Dav
APPLICANT: MU, RAY
TITLE OF INVENTION: RIC
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE: FEATURE: Description of Artificial Sequence:expression OTHER INFORMATION: cassette comprising a plant promoter linked to OTHER INFORMATION: intron, a sequence encoding an AMPA acetyl OTHER INFORMATION: transferase, and a termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: promoter LOCATION: (28)..(965)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: transit_peptide LOCATION: (1440)..(1667)
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ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1668) .. (2099)
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                                                                              STREET: CLINTON SQUARE, P.O. BOX CITY: ROCHESTER STATE: NEW YORK
                                                          COUNTRY: USA
                                                                                                                                          ADDRESSEE: NIXON,
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                                                                                                                                          HARGRAVE, DEVANS & DOYLE LLE
                                                                                                                                                                                                                                        David
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0

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; Patent No. 5641876
; GENERAL INFORMATION:
APPLICANT: MCBLICOY, I
APPLICANT: Wu, Ray
TITLE OF INVENTION: F
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NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 1960
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1536
TELEPHONE: 716-263-1560
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                   APPLICATION NUMBER: US/08/144
FILING DATE: 27-OCT-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 1960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
                                             TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/144,602B
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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CLASSIFICATION: 536
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ROCHESTER STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
STRANDEDNESS:
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                                LENGTH:
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               : 2199 base pairs nucleic acid
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CLINTON SQUARE, P.O. BOX 1051
                                                                                                                                                                                                                                                                                                                                                                                                      USA
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Pred. No. 9.2e-2
                                                                                                                                             19603/10140
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cheв 0;
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; TOPOLOGY: li
; MOLECULE TYPE:
US-08-144-6028-5
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Best Local Similarity
Matches 70; Conserv
                                                                                                                    Query Match 14.1%; Score 70; Best Local Similarity 100.0%; Pred. No. Matches 70; Conservative 0; Mismatch
                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5643 base pairs
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/
PILING DATE: 27-OCT-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,10
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: McElroy,
APPLICANT: Wu, Ray
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HP
                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 716-263-1636
                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: ROCHESTER STATE: NEW YORK
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                                                                                                                                                                                                                                            TYPE: nucleic acid
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                                                           809 TACTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGG
                                                                           356 TACTCGACGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGG
698
                              416 TAAGATTACC 425
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 TAAGATTACC 878
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                                                                                                                                        DB 1; Length 5643; 9e-26;
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RESULT 7 US-08-144-602B-6

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Sequence 6, Application US/08144602B Patent No. 5641876

GENERAL INFORMATION:

RICE ACTIN GENE AND PROMOTER 27

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RESULT 8
US-09-068-101-5
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Matches
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Patent No. 6372960
                                                                                                         SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                      CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: EP 96202446.9
EARLIER FILING DATE: 1996-09-03
NUMBER OF SEQ ID NOS: 10
SOFTMARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                APPLICANT: PLANT GENETIC SYSTEMS N.V. TITLE OF INVENTION: Improved Barstar Gene FILE REFERENCE: 2121-139P
                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/068,101
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APPLICANT: Wu, Ray
TITLE OF INVENTION: RIGI
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                               TYPE: DNA
ORGANISM: Artificial Sequence
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OTHER INFORMATION: Description of OTHER INFORMATION: acid, "plasmid
                                        FEATURE:
                                                                                     LENGTH: 4032
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APPLICATION NUMBER: US/08/144,602B
FILING DATE: 27-OCT-1993
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 191
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
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NAME: TIMIAN, SUSAN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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OPERATING SYSTEM: PC-DOS/MS-DOS
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BOX 1051
Artificial Sequence: other nucleic pMV71"
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; NAME/KBY: misc feature
; LOCATION: (4016)..(4021)
; OTHER INFORMATION: label = KpnI, "KpnI recognition site"
US-09-068-101-5
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Matches 6
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 5
                                                       NAME/KEY: misc_feature
LOCATION: (3677)..(4003)
OTHER INFORMATION: label = 3
OTHER INFORMATION: end of n
OTHER INFORMATION: "-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/970,921
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 2428-0108P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Frank Michiels et al.
TITLE OF INVENTION: Improved Barstar Gene
                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 40
TYPE: DNA
                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: other nucleic OTHER INFORMATION: acid, "plasmid pMV71"

NAME/KEY: misc_feature
LOCATION: (1999)..(3400)

OTHER INFORMATION: label = PRAC1, "promoter region of rice actin generates in the leader"
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LOCATION: (1993). (3400)
OTHER INFORMATION: label = PRAC1, "promoter region of rice actin gene
OTHER INFORMATION: - contains an intron in the leader"
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (3399)..(3404)
OTHER INFORMATION: label =
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OTHER INFORMATION: label :
OTHER INFORMATION: end of
OTHER INFORMATION: T-DNA"
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OTHER INFORMATION: label = barstar, "barstar DNA"
LOCATION: (3399)..(3404)
OTHER INFORMATION: label =
                      NAME/KEY: misc_feature
LOCATION: (3399)..(340
                                                                                                                                                                   LOCATION: (340\overline{1})...(3676)
OTHER INFORMATION: label = barstar, "barstar DNA"
                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (3401)..(367
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LOCATION: (3401)..(367)
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100.0%; Pr
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NcoI,
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                                                                               "region containing 3' untranslated ne synthase gene of Agrobacterium
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  "NcoI recognition site"
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; LOCATION: (4016)..(4021)
; OTHER INFORMATION: label = KpnI,
US-09-970-921-5
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US-09-682-597A-5
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APPLICANT: Chen, Guilan
APPLICANT: Hironaka, Catherine
APPLICANT: Firenaka, Catherine
APPLICANT: About Hironaka, Catherine
APPLICANT: Chen, Guilan
TITLE OF INVENTION: Glyphosate Tolerant Wheat Plant 33391 and Compositions and Method
TITLE OF INVENTION: Detection Thereof
FILE REFERENCE: 38-21(52232)A
CURRENT APPLICATION NUMBER: US/09/682,597A
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 399
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
            APPLICANT: Monsanto Technology LLC
APPLICANT: Chen, Guilan
APPLICANT: Hironaka, Catherine
APPLICANT: Zhou, Hua-Ping
TITLE OF INVENTION: Glyphosate Tolerant Wheat Plant 33391 and Compositions and Method
TITLE OF INVENTION: Detection Thereof
FILE REFERENCE: 38-21(52232)A
CURRENT APPLICATION NUMBER: US/09/682,597A
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
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LOCATION: (1)...(399)
OTHER INFORMATION: chimeric sequence of wheat genome and transgene insert
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es 63; Conserv
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PatentIn
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100.0%; Pred. No. 3.1e-24;
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100.0%; Pred. No. 3.6e-22;
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; ORGANISM: Oryza sativa
US-09-682-597A-2
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; FEATURE:
; NAME/KEY: SOURCE
; LOCATION: (1)..(29)
; OTHER INFORMATION: fully synthesized
US-09-872-051-4
APPLICANT: MODERANTO CO
APPLICANT: Behr, Carl
APPLICANT: Hironaka, Catherine
APPLICANT: Hironaka, Catherine
APPLICANT: Hock, Gregory
APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and
TITLE OF INVENTION: Thereof
FILE REFERENCE: 38-21(5258)B
CURRENT APPLICATION NUMBER: US/09/872,051
CURRENT APPLICATION NUMBER: 05/01/872,051
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR FILING DATE: 2000-06-22
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APPLICANT: Behr, Carl
APPLICANT: Hironaka, Co
APPLICANT: Heck, Gregod
APPLICANT: You, Jinsonc
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/241,215
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/240,014
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 2000-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Heck, Gregory
APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Det
TITLE OF INVENTION: Thereof
FILE REFERENCE: 38-21(52258)B
FILE REFERENCE: 38-21(52258)B
CURRENT APPLICATION NUMBER: US/09/872,051
CURRENT APPLICATION NUMBER: US/09/872,051
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR FILING DATE: 2000-66-22
PRIOR FILING DATE: 2000-66-22
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TYPE: DNA
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100.0%; Pr
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100.0%; Pred. No.
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hes 0;
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9e-05;
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US-09-441-340-29
Sequence 29, Application US/09441340
Patent NO. 644876
GENERAL INFORMATION:
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; Sequence 14, Application US/09872051
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                                                                                      RESULT 15
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                                                                                                                                                                                                                                                                                     ; NAME/KEY: SOUTCE
; LOCATION: (1)..(22)
; OTHER INFORMATION: fully synthesized
US-09-872-051-14
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                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0 SEQ ID NO 14 LENGTH: 22
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/213,567
PRIOR ETLING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/240,014
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 38-21(52258)B
CURRENT APPLICATION NUMBER: US/09/872,051
CURRENT FILING DATE: 2001-06-01
APPLICANT: Barry, Gerard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Heck, Gregory
APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Detection of Invention: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/241,215
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/240,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Monsanto Co
APPLICANT: Behr, Carl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 16
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ORGANISM: Artificial
FEATURE:
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LOCATION: (1)..(22)
OTHER INFORMATION: fully synthesized
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100.0%; Pred. No.
/ative 0; Mismatcl
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Search completed: February 10, 2005, 08:49:45

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                                                                                    Query Match
Best Local 9
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LENGTH: 2107
                                                                      Matches
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CURRENT APPLICATION NUMBER: US/09/441,340
CURRENT FILING DATE: 1999-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 60/108,763
EARLIER FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                     FEATURE: terminator LOCATION: (1869)..(2102)
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: promoter LOCATION: (26)..(590)
                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (1427)..(1858)
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                       337 GCGGCCGCGTTAACAAGCTT 356
1 GCGGCCGCGTTAACAAGCTT 20
                                                                    l Similarity 100.0%; Pred. No. 3. 20; Conservative 0; Mismatches
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(615)..(685)
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1: geneseqn1980s:*
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1183
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

20	19	18	17	c 16	15	14	13	12	c 11	c 10	ი 9	ი 8	c 7	ი 6	ი წ	c 4	ი ა	ი 2	1	Result No.
147	147	147	147	147	147	159	163	163	168	169	169	169	171	171	171	171	171	202	1183	Score
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3754	3754	3754	1360	896	349	474	10003	6865	4032	11643	7545	5118	9359	9359	2181	1501	1501	2378	1183	Query Match Length
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ABX95186	AAD61790	AAZ51642	AAD51480	ADP83767	AAD51491	ADP83768	AAF80295	AAF80287	AAV23237	ACF58344	ACF58343	ADP73930	ABK10687	ABK11039	ADC84543	AAC89325	AAC87194	AAD01016	ABK15245	ID
Abx95186 B. thurin	Aad61790 Bt.cry3Bb	Aaz51642 Bacillus	Aad51480 Consensus	Adp83767 Bentgrass	Aad51491 A. tumefa	Adp83768 Bentgrass	Aaf80295 Nucleotid	Aaf80287 Nucleotid	Aav23237 Plasmid p	Acf58344 Nucleotid	Acf58343 Nucleotid	Adp73930 Plasmid p	Abk10687 Transform	Abk11039 pVDH636 v	Adc84543 Rice acti	Aac89325 Rice acti	Aac87194 Rice acti	Aad01016 Expressio	Abk15245 Corn nk60	Description

### ALIGNMENTS

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ds; rice actin 1 promoter; RA1; RA1 intron; chloroplast transit peptide gene; glyphosate resistance; corn; 5-enol-pyruvylshikimate-3-phosphate synthase; EPSPS; Hsp70 intron; transcriptional terminator; cauliflower mosaic virus 35S promoter; pv-ZMGT32; transgenic; nk603.
                                                                                            misc_feature
                                                                                                                                                      misc_feature
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Agrobacterium tum
Synthetic.
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22-JUN-2000; 2000US-0213567P
                   15-JUN-2001; 2001EP-00202314
                                      02-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a DNA construct (I) comprising a first (F1) and CC a second (F2) expression cassette. F1 of the DNA construct, in operable CC linkage, has rice actin 1 (RA1) promoter, RA1 intron, chloroplast transit peptide gene (II), glyphosate tolerant 5-enol-pyruvylshikimate-3-CC (IV), and F2 has cauliflower mosaic virus 35S promoter, Hsp70 intron, CC (IV), and F2 has cauliflower mosaic virus 35S promoter, Hsp70 intron, CC (II), (III) and (IV). Also included are two DNA sequences from corn plant PV-ZMGT32(nk603) of 498 or 1183bp, or primers and probes derived from CC them (used to detect transgene junction points). The construct is useful for producing a corn plant that tolerates application of glyphosate CC herbicide by transforming a corn cell with, selecting the corn cell into a CC tolerance to application of glyphosate, and growing the corn cell into a CC tolerance to application of glyphosate, and growing the corn cell into a CC consisting of the Agrobacteium transcriptional terminator sequence, vector sequences and corn sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 1183; Conserv
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13-OCT-2000;
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                                                   TATCAAGCTTGGTACCACGCGACACACTTCCACTCTAGTGTTTGAGTGGATCCTGTTATC
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2000US-0241215P.
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               CAGCGCCCAGAGAGAAAAAAAAGGAAAGGAAGGCGCGAGATGATG
                                                                                                                    GCTCTGCGCAAATCACGAAGAACCAGTGGGGCCGCTCGCGCCTAGGCCCACCGCCAGGAGC
                                                                                                                                                                                                                                                                                  GACGACGTAGGCAGGGGTGGCCATAACGACGGTGGCGGCATCCAACTTGTTCTTTCCCTT
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 CAGCGCCCAGAGAGAAAAAAAGGAAGGAAGGCGCGAGATGATG
                                                                     GGGGCTTGTTGCGAGCCGTAGCGTCGGGAAGGGGACGACCCGCTAGGGGGGCCCATGCTC
                                                                                                       GCTCTGCGCAAATCACGAAGAACCAGTGGGGCCCTCGCCGCCTAGCCCACCGCCAGGAGC
                                                                                                                                                                         GGTCGCGGGGCCCGATTTTTATAGCCTGGGCGAGGACCGAGCTTGGCCGAACCGATCCAGA
                                                                                                                                                                                                                                 TCTCTGTCTTCAACTTGCGCCGGCAGTCTGCTAGACCCCAGGGGATGCTGTGTGGAGGAGA
                                                                                                                                                                                                                                                                    GACGACGTAGGCAGGGGTGGCCATAACGACGGTGGCGGCATCCAACTTGTTCTTTCCCTT
                                                                                                                                                                                                                                                                                                                       TTCAACACGGTCGCGACACGGATGCAACGGACCCTCCAAGCCAATACTCGAGGCCGGACC
                                                                                                                                                                                                                                                                                                                                     TTCAACACGGTCGCGACACGGATGCAACGGACCCTCCAAGGCCAATACTCGAGGCCGGACC
                                                                                                                                                                                                                                                                                                                                                                            ATAAAATGGACAACAACACCCTGCCCTTCACTACCGGTCGGAGCGACGCCGAAGATGGGG
                                                                                                                                                                                                                                                                                                                                                                                            ATAAAATGGACAACAACACCCTGCCCTTCACTACCGGTCGGAGCGACGCCGAAGATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                ATAGGTGTTACATCGCGTATACAACTTAACCGTACACCACTTTTAGCAATGGCTCGTAAT
                                                                                                                                                                                                                TCTCTGTCTTCAACTTGCGCCGGCAGTCTGCTAGACCCAGGGGATGCTGTGTGGAGGAGA
                                                   IGTTGCGAGCCGTAGCGTCGGGAAGGGGACGACCCGCTAGGGGGGGCCCATGCTC
                                                                                                                                                             ATAGCCTGGGCGAGGACGAGCTTGGCCGAACCGATCCAGA
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RESULT 2
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ID AADO1016;
XX AADO1016;
AC AADO1016;
XX DT 21-SEP-200
XX Expression
XX Phosphonat
XX Phosphonat
XX Ecorn; toba
XX CORP; glyph
XX Secherichi
OS Synthetic.
XX Escherichi
OS Synthetic.
XX Key
FT promoter
FT intron
FT intron
FT transit_pe
FT transit_pe
                                                                                                                                                                                                            acyltransferase; transacylase; recombinant plant; expression cassette; corn; tobacco; wheat; cotton; canola; rice; chloroplast transit peptid CTP; glyphosate oxidase; GOX; glyphosate oxidoreductase; phno gene; self-fertilisation; hetero-fertilisation; ds.
                                                                                                                                                                                                                                                                                                             Expression
               transit_peptide
                                                                                                                                                                Synthetic
                                                                                                                                                                              Escherichia
                                                                                                                                                                                                                                                                             Phosphonate herbicide tolerance; aminomethyl phosphonic acid; AMPA; AAT;
                                                                                                                                                                                                                                                                                                                                               21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                           standard; DNA; 2378
                                                                                                                                                                                                                                                                                                            cassette-3 comprising modified E. coli P2A phnO coding
                                                                                                                                                                                coli.
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                                                              /*tag= a
/note= "Plant
966. .1423
               /note= "Enhances
1440. .1667
                                                                                                                               Location/Qualifiers
                                                *tag=
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peptide;

heterologous

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                                                                                                                                                                                                                                                                                                                      CC herbicide tolerance in recombinant corn, tobacco, wheat, cotton, canola CC and rice plants, by transforming the plants with an expression cassette. CC It comprises of a structural DNA sequence, that encodes an aminomethyl CC phosphonic acid (AMPA) acyltransferase or transacylase (AAT), capable of CC N-acylation of AMPA. This sequence has an amino terminal chloroplast CC transit peptide (CTP), that targets AAT to the chloroplast. Co-expression CC diplyphosate oxidase (GOX) gene, encoding glyphosate oxidoreductase, CC along with AAT provides the transformed plants with higher resistance to CC phosphonate herbicides. This method is useful for enhancing phosphonate CC and to prevent self-fertilisation and enhance hetero-fertilisation. The CC operable promoter and 5' sequences like intron, linked to modified E. CC coli phno coding region, encoding P2A AMPA acyltransferase (AAT) enzyme CC and plant operable termination sequences
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enhancing phosphonate herbicide tolerance in corn, tobacco, wheat, cotton, canola and rice plants involves transforming plants with phosphonate metabolizing genes encoding acyltransferase enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The patent discloses a method for selectively enhancing the phosphonate herbicide tolerance in recombinant corn, tobacco, wheat, cotton, canola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-387806/33
P-PSDB; AAY71251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 167-169; 179pp; English.
                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                   Local Similarity
                                                                                     283
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22
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                                                                                                                                       ACTTTATACCACCTTTTAACTGATGTTTTCACCTTTTGACCAGGTAATCTTACCTTTGTTT
                                                                                                                                                                          TTTTATAATAGTAGAAAAGAGTAAATTTCACTTTGGGCCACCTTTTATTACCGATATTTT
                                                           ACTITATACCACCTITTAACTGATGTTTTCACTTTTGACCAGGTAATCTTACCTTTGTTT
                 ACGCGGCCGCCCTAGGGATATC
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                 BP; 604 A; 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /.u..ction= "Transfers acyl group from an acylcarrier (CoA) to the free amino group of aminomethylphosphonate" 2114. .2369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organelle,
1668. .210
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/function= "Transfers acyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Targets the protein to an intracellular
organelle, like chloroplast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Escherichia coli modified P2A AMPA
psyltransferase (AAT) enzyme"
                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                     17.1%;
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%; Pred. No. 8.7
0; Mismatches
                                                                                                                                                                                                                                                                                                  C; 552 G;
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AC AAC871
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AC AAC871
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Rice B
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                 Containing two amino acid substitutions relative to the corresponding CC wild-type region (AAB29792). The invention also encompasses plant genomic CC EBSPS sequences identified via screening with a rice EBSPS intronic CC sequence; vectors and host plant cells comprising a nucleic acid sequence of the invention; transgenic plants (and tissues and seeds thereof) CC comprising a nucleic acid sequence of the invention, pationally further CC transformed with a DNA encoding an insect, fungal, viral bacterial, CC producing the transgenic plants of the invention. The nucleic acid sequence of tree invention and methods of CC constructs of the invention are used to produce a wide variety of CC constructs of the invention are used to produce a wide variety of CC constructs of the invention are used to produce a wide variety of CC constructs of the invention are used to produce a wide variety of CC constructs of the invention are used to produce a wide variety of CC constructs and canola, glyphosate resistant plants. The glyphosate turf and forage grasses and nut-producing plants. The glants are CC optionally resistant to insects, fungi, viruses, bacteria, nematodes, CC stress, desication and/or other herbicides. The plants are production of a herbicidal target for the high throughput in vitro CC enhancer element which may be used in the rice EBSPS expression cassette of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rice EPSPS; 5-enolpyruvylshikimate phosphate glyphosate resistance; herbicide resistance; expression construct; enhancer element; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to rice 5-enolpyruvylshikimate phosphate synthas (EPSPS) genomic DNA (AAC87188). The invention also relates to an expression cassette comprising, in the 5'-3' direction, one or more transcriptional enhancer elements selected from AAC87190-C87196), the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rice actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC87194 standard; DNA; 1501 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rice EPSPS promoter, genomic DNA encoding a rice EPSPS chloroplast transit peptide, genomic DNA encoding a EPSPS protein modified such that it is resistant to glyphosate (AAC87189), and a transcriptional terminator. The glyphosate resistant EPSPS contains a region (AAB29793)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 19; Page 55-56; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotide encoding 5-enolpyruvylshikimate phosphate synthase, used to produce transgenic plants e.g. banana, wheat, maize or rice, having resistance or tolerance to glyphosate herbicide.
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99GB-00017847.
99GB-00030200.
99GB-00030204.
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99GB-00030209
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RESULT 4

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Best Local Sim
Matches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-1999;
29-JUL-1999;
21-DEC-1999;
21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-APR-1999;
29-APR-1999;
29-APR-1999;
                                                                                                                                                                                                                                                    Isolated
synthase
                                                        The present invention relates to an Oryza sp. 5-eno phosphate synthase (EPSPS) gene. Vectors containing to produce plant tissues and fertile whole plants whole results to substantially resistant to syphosate he produce a herbicidal target which is used for high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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29-JUL-1999;
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                                         screening
                                                                                                                                                                                          Example
                                                                                                                                                                                                                                 resistance
                                                                                                                                                                                                                                                                                                                                                          Hawkes
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                                                                                                                                                                                                                                                                                                                                                                                                   ZENECA
                                                                                                                                                                                                                               polynucleotide encoding a 5-enolpyruvylshikimate phosphate from rice is used for producing transgenic plants with enhanced ce to glyphosate herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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                                           ō,
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                                                                                                                                                                                     Page
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                                                                                                                                                                                                                                                                                                                                                          Warner SAJ,
                                           potential
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99GB-00017836.
99GB-00017843.
99GB-00030202.
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                                                                                                                                                                                                                                                                                                                                                          Andrews
                                                                                                                                                                                     English.
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Pred. No.
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                                                                             containing the gene may be used le plants which are substantially lyphosate herbicide and to
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                                                            throughput in vitro
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966 222 Query Match Best Local S Matches 171

Similarity

14.5%; but 100.0%; Pr

Score 171; DB; Pred. No. 2.3

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Sequence

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RESULT 5
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ID ADC845
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Matches
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                 The present invention relates to an invention that results in the expression of the endogenous nucleotide sequence in plant cell being increased. In this method the plant cell comprises a second expression cassette comprising a nucleic acid molecule, where the expression of the nucleic acid molecule of interest in the plant cell is decreased as compared to expression of the nucleic acid molecule of interest in a plant cell lacking the first expression cassette. The methods and compositions of the present invention are useful in molecular biology stransformation, in particular for reproducing and predictably manipulating gene expression in a plant cell. The present sequence is smucleotide sequence of rice actin promoter.
                                                                                                                                                                           Disclosure; Page 106-107; 108pp; English.
                                                                                                                                                                                                                New isolated nucleic acid molecule encoding a polypeptide with a exonuclease domain, useful in molecular biology and transformatic particular for reproducing and predictably manipulating gene expr
                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2002;
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                                                                                                                                                                                                                                                                                            Levin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression
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                                                                                                                                                                                                       cell.
                                                                                                                                                                                                                                                                                           Dietrich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               promoter encoding
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
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                                                                                                                                                                                                                                transformation,
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                                                                                                                                                                                                                 mation, in expression
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RESULT 6
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ABKI11039/c
ID ABKI10
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AC ABKI10
DT 05-JUN
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VDDH63
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VDDH6
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27-NOV-2000;
27-NOV-2000;
22-JUN-2001;
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                    The invention relates to a grass plant, which has been genetically modified to substantially inhibit generative propagation and carry herbicide resistance. The grass is useful for growth and/or propagation of grasses. The grass is used to play at least one sport (e.g. baseball, cricket, football, golf, rugby, soccer or tennis), or used at least in a portion of an athletic field, lawn or park. The grass is fed to animal feedstuff. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                                             propagation, feedstuff) o
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                                                                                                                                                                                                                                                                                        genetically modified grasses that express inhibited generative pagation, or herbicide resistance, useful for forage (e.g. cattle detuff) or amenity purposes (e.g. for use in an athletic field, lawn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mays
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)B; AAU76514.
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1; cricket; football; golf; rugby; soccer; tennis; lawn; park;
c field; animal feedstuff; grass flowering inhibitor; AtH1; ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Valk
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                                                                                                                                                                                                                     Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000US-0253274P.
; 2000US-0253327P.
; 2001US-0300220P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ָט,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001WO-EP009572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0226422P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "AtH1"
/partial
/note= "No stop c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEEDS BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
4930. .6360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
     at, horse or sheep) or
represents the coding
                                                                                                                                                                                                                  56pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9359
                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CMP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis AtH1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smeekens SCM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proveniers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wn; park;
AtH1; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333
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sequence of

pVDH636

The invention relates to a grass plant which modified to substantially inhibit generative

has been genetically propagation. The gen

genetic

Fig

6,

English.

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RESULT 7
ABK10687/c
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밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          containing in grasses
                                                                                                                                                                                                                                                                                                                             Grass; plant; transgenic; flowering inhibition; inflorescence; gene; tiller production; delayed heading; gibberellic acid; phytohormone; genetically modified grass; athletic field; sport; baseball; cricket football; rugby; soccer; tennis; lawn; landscaping; cattle; horse; goat; animal feedstuff; Arabidopsis thaliana; AtHI; homeobox gene;
                                                                                                                                                      18-AUG-2000;
27-NOV-2000;
27-NOV-2000;
22-JUN-2001;
                                           New genetically modified grass useful grass in athletic fields (for sports s golf, rugby, soccer and tennis), or as horse and sheep.
                                                                                                                  Van
                                                                                                                                                                                                                                       WO200214486-A2
                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                       Transformation
                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                            ABK10687;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK10687
                                                                                         P-PSDB;
                                                                                                                                                                                                    16-AUG-2001; 2001WO-EP009570
                                                                                                                                     (ADVA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6798
                                                                                                                   Der Valk P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                     ADVANTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTTTATACCACCTTTTAACTGATGTTTTCACTTTTGACCAGGTAATCTTACCTTTGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                      ; 2000US-0226422P.
; 2000US-0253274P.
; 2000US-0253327P.
; 2001US-0300220P.
                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis AtH1 gene,
                                                                                                                                                                                                                                                                                                                                                                                      vector plasmid pVDH636 DNA.
                                                                                                                                                                                                                                                                          Location/Qualifiers
4930. .6351
                                                                                                                                     SEEDS
                                                                                                                                                                                                                                                         /*tag= a
/product= "Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2377
                                                                                                                   Van
                                                                                                                                                                                                                                                                                                                        pVDH636.
                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                    ified grass useful for growing and/or propagating ields (for sports such as baseball, cricket, footl and tennis), or as animal feedstuff for cattle, ?
                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.5%;
                                                                                                                    Dun
                                                                                                                                      ΒV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,
                                                                                                                                                                                                                                                                                                                                                                                                                                              9359
                                                                                                                   CMP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 171;
Pred. No.
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                                                                                                                     Smeekens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which was used to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ດ
                                                                                                                     SCM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.2e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
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                                                                                                                     Proveniers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8899
                                                                                                                                                                                                                                                                                                                                                    cricket;
                                                                                                                                                                                                                                                                                                                                                                       gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       flowering
                                                                                                                                                                                                                                                                                                                                                              ; ds;
golf;
                                                       goat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6799
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ADP73930/c
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        making a grass involves transforming the grass with a nucleic acid which interferes with metabolism of gibberellic acid. A grass can be treated by applying a phytohormone to at least partially relieve or reverse a change in plant characteristic resulting from genetic modification. The genetically modified grass is useful for growing and/or propagating grass in athletic fields (for sports such as baseball, cricket, football, golf, rugby, soccer and tennis), lawns, parks and other types of landscaping. The grass is also useful as an animal feedstuff for cattle, goats, horses and sheep, due to its increased vegetative growth, improved digestibility and/or nutritional value as animal feedstuff. This sequence represents plasmid pVDH636 DNA. This plasmid was used as a transformation vector for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modification may result in a heritable change in one or mor characteristics such as inhibition of flowering (or substan that amounts to inhibition), absence of inflorescence, incr production of tillers, delayed heading and inhibition of the developmental switch from vegetative to generative growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic plant; immunoglobulin production; recombinant production; glycosylation; fucose; glycan; virucide; immunotherapy; maize; lipas 3'UTR; rice; actin promoter; phosphinothricin acyltransferase; PAT; plasmid; pDAB3014; cyclic; circular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9359 BP; 2377 A; 2222 C; 2133 G; 2624 T; 0 U; 3 Other;
                                                                                                                              3'UTR
                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                            promoter
                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pDAB3014,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP73930 standard; DNA; 5118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 production of transgenic grasses expressing the Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                         Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTTTATACCACCTTTTAACTGATGTTTTCACTTTTGACCAGGTAATCTTACCTTTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTATAATAGTAGAAAAGAGTAAATTTCACTTTTGGGCCACCTTTTATTACCGATATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTTTATACCACCTTTTAACTGATGTTTTCACTTTTGACCAGGTAATCTTACCTTTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTTATAATAGTAGAAAAGAGTAAATTTCACTTTGGGCCACCTTTTATTACCGATATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
been de
as the
6652"
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                   /note= "Maize lipase 3'UTR. The 3' end of this 3'UTR has been deduced from that given for pDAB8505 (SEQ ID NO:85) as the 3'UTR location given for this plasmid is 2296-
                                                                                                                                                                                                         note= "Rice actin
727. .2281
                                                                                                                                                  product= "Phosphinothricin acyltransferase (PAT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.5%;
                                                                                                                              .2627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s inhibition of flowering (or substantial of tion), absence of inflorescence, increased delayed heading and inhibition of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a heritable change in one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 171;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             쁑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                  promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.2e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 9359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lipase;
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멍 Ś 밁 Ś 밁 S

Nucleotide sequence of plasmid pDAB8504.

GnTIII; N-acetylglucosaminyltransferase; transgenic; glycoprotein;

g

282 437

0

377

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ACF58343/c
ID ACF583
XX
AC ACF583
XX
DT 12-FEB
XX
DE Nucleo
XX
GnTIII
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                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody. The invention also relates to constructs plasmids and vectors of producing the immunoglobulins; transformed plant cells, calli, plant cissues and whole plants for producing the immunoglobulins; the immunoglobulins methods for producing the immunoglobulins. The immunoglobulins of the invention may be used to treat HSV infection or tumour angiogenesis. The invention may be used to treat HSV infection or tumour angiogenesis. The invention comproduction, reduced costs, and elimination of pathogenic contaminants such as viruses and prions, with a simplified (i.e., non-plant-specific) glycosylation profile which reduces the risk that the immunoglobulin may not be functional in animals. The present sequence represents the plasmid pDAB3014, which may be used in the invention. The plasmid contains a phosphinothricin acyltransferase (PAT) gene under the control of a rice actin promoter, and a maize lipase 3'UTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      Matches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Briggs K,
Pareddy D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel plant-produced immunoglobulin having glycopeptide or glycan profile with reduced fucosylation, useful for treating herpes simplex virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DOWC )
                                                                                                 ACF58343;
                                                                                                                               ACF58343 standard; DNA; 7545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5118 BP; 1240 A; 1256 C; 1286 G; 1336 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the production of immunoglobulins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 69; SEQ ID NO 84; 212pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-NOV-2002; 2002US-0429385P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-NOV-2003; 2003WO-US037905
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                                                                  12-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fucose. The immunoglobulins produced can be of any class (i.e., IgM, IgE or IgD) and is especially an anti-herpes simplex virus antibody or an anti-alphavbeta3, alphavbeta5 dual integrin
                                                                                                                                                                                                                376
                                                                                                                                                                                                                                                                           436
                                                                                                                                                                                                                                                                                                                                          496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOW CHEM CO.
DOW AGROSCIENCES LLC
EPICYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Petolino
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                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     14.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rubin-Wilson B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ç
                                                                                                                                                                                                                                                                                                                                                                                                      Score 169; DB 12;
; Pred. No. 2.2e-73;
0; Mismatches 0;
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Taylor D, Roberts JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson WHK;
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter
The invention relates to a plant host cell system comprising a mammalia UDP-N-acetylglucosamine: beta, D mannoside beta \{1,4\}-N-acetylglucosaminyltransferase (GnTIII) enzyme, a nucleic acid sequence encoding a mammalian GnTIII protein, or a vector comprising the GnTIII
                                                                                                                                                                                                              WO2003078614-A2
                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                        misc_feature
                                                                 New plant host cell system for producing a desired glycoprotein compra
a mammalian N-acetylglucosaminyltransferase (GnTIII) enzyme, a nucleic
acid sequence encoding the enzyme, or a vector comprising the nucleic
                                                                                                                                                    19-MAR-2002;
26-MAR-2002;
                                          Example 6;
                                                                                                   WPI;
                                                                                                                   Bakker HAC,
                                                                                                                                                                              18-MAR-2003; 2003WO-IB001562
                                                                                                                                    (PLAN-)
                                                           sequence.
                                                                                                   2003-779132/73.
                                                                                                                                     PLANT
                                          Fig
                                                                                                                   Florack DEA,
                                                                                                                                                     2002US-0365769P
2002US-0368047P
                                                                                                                                     RES
                                          7B;
                                                                                                                                                                                                                                                                                                                                                   4837.
                                                                                                                                                                                                                                                                                                                                                                                               /worden "maize lipase UTR"

complement(3671. .4836)

/*tag= 4
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                                                                                                                                                                                                                                                                          5130.
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                                                                                                                                                                                                                                                                                                                                                                                                             /mote= "maize lipase
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "linker sequence (ACF58352)"
3273. .3629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "linker"
                                                                                                                                                                                                                                                        note= "Puc19"
                                                                                                                                                                                                                                                                                                note= "Puc19"
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                                                                                                                                                                                                                                                                                                                                                            note= "linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "PAT gene"
259. .3272
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                                                                                                                                                                                                                                                                                 note= "linker sequence
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                                          English.
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                                                                                                                                                                                                                                 (ACF58356) "
                                                                                                                                                                                                                                                                                                                                    (ACF58354) "
                                                                                                                                                                                                                                                                                                                                                            (ACF58353)"
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Matches 169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid. The plant host system is useful in producing a desired glycoprotein or its functional fragment. The glycoprotein or its functional fragment may be used for the production of a pharmaceutical composition. The present sequence represents the nucleotide sequence plasmid pDAB8504
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                                                                                                                      promoter
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                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                              GnTIII; N-acetylglucosaminyltransferase;
                                                                                                                                                                                                                                                                                                                                                Nucleotide
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              misc_feature
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                                                                                                                                                                                                                                                                                                                                                 sequence
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                                                                                             /notes "rice actin 6803. .7358
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                /note= "maize
7730. .7770
                                                                                                                                                                                                              note= "maize
                                                                                                                                                                                                                                        note= "linker sequence"
                                          note= "linker sequence 373. .7729
                                                                  'note= "PAT v3"
1359. .7372
                                                                                                                                note= "multiple
                                                                                                                                                                                      note= "GNTIII v.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2128 A; 1579 C; 1622 G; 2216
                                                                                                                                                                                                                                                                                                                                                                                                    DNA; 11643
                                                                                                                                                                                                                                                                                     .1164
                                                                                                                                                                                                                                                                                                                                                 of plasmid pDAB7113
                                                                                                                                                                                                                                                                                                                                                                  entry)
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                                                                                                                      .6802
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                                                                                                                                                           "maize
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"linker sequence (ACF58360)"
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Pred. No.
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                                                                                                                                cloning sites
                                                                                                      promoter v2"
                         UTR"
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                                                                                                                                                                                                                                         (ACF58357) "
                                                  (ACF58359) "
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                                                                                                                                                                                                                                                                                                                              transgenic; glycoprotein;
                                                                                                                                                                                                               promoter'
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                                                                                                                                 (ACF58358) "
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RESULT 11
AAV23237/c
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XX
AC AAV23
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T7-JT
DT 17-JT
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DT 17-JT
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DB Plasn
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Best Local S
Matches 169
                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a plant host cell system comprising a mammalian UDP-N-acetylglucosamine: beta-D mannoside beta(1,4)-N-acetylglucosamine) beta-D mannoside beta(1,4)-N-acetylglucosaminyltransferase (GnTIII) enzyme, a nucleic acid sequence encoding a mammalian GnTIII protein, or a vector comprising the GnTIII nucleic acid. The plant host system is useful in producing a desired glycoprotein or its functional fragment. The glycoprotein or its functional fragment may be used for the production of a pharmaceutical composition. The present sequence represents the nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New plant host cell system for producing a desired glycoprotein comprises a mammalian N-acetylglucosaminyltransferase (GnTIII) enzyme, a nucleic acid sequence encoding the enzyme, or a vector comprising the nucleic acid sequence.
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Barstar; barnase inhibitor; plasmid pMV71; circular; ds.
                                                                                                                         237/c
                                                                                                                                                                                                                                                                                                                                                                     Sequence 11643 BP;
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                                   Plasmid pMV71.
                                                             17-JUL-1998
                                                                                     AAV23237;
                                                                                                             AAV23237
                                                                                                                                                                                                                                                                                                                                                                                           plasmid pDAB7113
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26-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PLAN-) PLANT
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                                                                                                                                                                                                                                                                                              163
                                                                                                                                                                                                                                                                                                                      169;
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                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                          ACTTTATACCACCTTTTAACTGATGTTTTCACTTTTGACCAGGTAATCTTACCTTTGTTT
                                                                                                                                                                                                                                                                                     TTTTATAATAGTAGAAAAGAGTAAAATTTCACTTTGGGCCACCTTTTATTACCGATATTTT
                                                                                                                                                                                                                       ACTTTATACCACCTTTTAACTGATGTTTTCACTTTTGACCAGGTAATCTTACCTTTGTTT
                                                                                                                                                                                                                                                                       TTTTATAATAGTAGAAAAGAGTAAAATTTCACTTTGGGCCACCTTTTATTACCGATATTTT
                                                                                                             standard;
                                                                                                                                                                        Fig 8B; 122pp;
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002US-0365769P.
2002US-0368047P.
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                                                           (first
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10164.
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                                                                                                            DNA; 4032 BP.
                                                                                                                                                                                                                                                                                                                                                                    3005 A;
                                                             entry)
                                                                                                                                                                                                                                                                                                                                 14.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                    2672 C;
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                                                                                                                                                                                                                                                                                                                      0
              fertility
                                                                                                                                                                                                                                                                                                                               Score 169; DB 10;
Pred. No. 2.1e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹3"
                                                                                                                                                                                                                                                                                                                      Mismatches
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              restoration;
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                                                                                                                                                                                                                                                                                                                                                                     3331
                                                                                                                                                                                                                                                                                                                                                                     T; 0
                                                                                                                                                                                                                                                                                                                                            Length 11643;
                                                                                                                                                                                                                                                                                                                      Indels
              male-sterile line;
                                                                                                                                                                                                                                                                                                                                                                    U; 0 Other;
                                                                                                                                                                        5405
                                                                                                                                                                                               331
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RESULT 12
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Best Local Sim
Matches 168;
                                                                          AAF80287;
                                                                                             AAF80287
                                                                                                                                                                                                                                                                                                Sequence 4032 BP; 1072 A;
                                                                                                                                                                                                                                                                                                                 The present sequence was used in the preparation of an improved Bac amyloliquefaciens barstar, i.e. barnase inhibitor, which can be use restrore fertility to male-sterile lines. The DNA sequence encoding improved barstar, leads to increased barstar production in tapetum due to improved translation, and possibly protein stability
                                                                                                                                                                                                                                                                                                                                                                           Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SdD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
          P382
                 Vector; transgenesis;
                                    Nucleotide sequence of plasmid pMRT1195
                                                        29-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                              male-sterile
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-193630/17
                                                                                                                                                                                                                                                                                                                                                                                                                                             Michiels F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PLBZ ) PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9810081-A2
                                                                                                                                            2046
                                                                                                                                                                                 2106
                                                                                                                                                                                                                      2166
        protein;
                                                                                                                                                                                                   223
                                                                                                                                                                                                                                         163
                                                                                                                                                             283
                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                           3; Page 37-39; 54pp; English.
                                                                                                                                                       ACTITATACCACCITTTAACTGATGTTTTCACTTTTGACCAGGTAATCTTACCTTTGTTT
                                                                                                                                                                                                                      TTTTATAATAGTAGAAAAGAGTAAATTTCACTTTGGGCCACCTTTTATTACCGATATTTT
                                                                                             standard;
                                                                                                                                            ACTITATACCACCITTIAACTGATGTTTTCACTTTTGACCAGGTAATCTTACCTTTGTTT
                                                                                                                                                                                                                                  TTTTATAATAGTAGAAAAGAGTAAATTTCACTTTGGGCCACCTTTTATTACCGATATTTT
                                                                                                                                                                                                                                                          14.2%; Score 168; DB 2; llarity 100.0%; Pred. No. 7e-73; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             an improved barstar protein plant lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Williams
                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENETIC
         antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-EP004739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96EP-00202446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= c
/note= "region containing
/note= of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product= "barstar"
677. .4003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "promoter region in the leader" 3401. .3676
                                                                                             DNA;
                                                        entry)
                 trfA locus; RK2 ori; oriV; P285 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEMS
                                                                                             6865
         resistance
                                                                                                                                                                                                                                                                                                 968 C; 963 G;
                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z
        gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        얁
                                                                                                                                                                                                                                                                                                 1029 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                         ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3' unstranslated end
Agrobacterium T-DNA"
        nptIII;
                                                                                                                                                                                                                                                                                                                                                                                                         used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rice
                                                                                                                                                                                                                                                                              2
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                                                                                                                                                                                                                                                                             Length 4032;
                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       actin gene
         transgenic
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                         restore
                                                                                                                                            1999
                                                                                                                                                                                                                                                                                                                                                                                                         fertility
                                                                                                                                                                                                                                                            <u>,</u>
         plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contains
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                                                                                                                                                                                                                                                                                                                                               Bacillus
used to
                                                                                                                                                                                                                                                                                                                                       used to
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                              cells,
                                                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                                                                                       2107
                                                                                                                                                                                  2047
                                                                                                                                                                                                     282
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                                                                                                                                                                                                                                          222
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The specification describes a synthetic vector containing only those elements essential for its functionality and transgenesis of a cell (especially a plant cell). The vector consists of at most one origin of replication (ori) at most one sequence encoding a selection agent and a trfA locus encoding a protein that increases the level of plasmid replication. The vector particularly contains an RK2 ori, especially oriver from pRK2 of Escherichia coli with a broad host range, an antibiotic resistance gene (especially nptIII conferring resistance to kanamycin in bacteria) and a trfA locus from pRK2 encoding the proteins p285 and p382. The vectors are used to prepare transgenic plants and transformed host cells for production of a heterologous proteins, e.g. insulin, interferon, lipase, blood proteins and anti-inflammatory agents. The present sequence represents a plasmid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rep_origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                         Gruber V, Comeau D;
                                                                                                                                                                                                                                                                                                                                                              03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                  09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rep_origin
                                                                                                                                                                                                               Claim 20; Page 128-131; 180pp; French.
                                                                                                                                                                                                                                                                               WPI; 2001-259847/27.
                                                                                                                                                                                                                                                                                                                                                                                        03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                             FR2798139-A1
                                                                                                                                                                                                                                                      New vector free from non-essential elements, useful for transforming
Sequence
                                                                                                                                                                                                                                                                                                                                   (MERI-) MERISTEM THERAPEUTICS
 6865
                                                                                                                                                                                                                                        protein production
BP;
                                                                                                                                                                                                                                                                                                                                                              99FR-00011112
                                                                                                                                                                                                                                                                                                                                                                                        99FR-00011112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
655. .1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphotransferase and kanamycin resistance"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "T-DNA left border"
4272. .4559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and P382 enabling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Bar gene coding for phosphinotricin
acetyltransferase and glufosinate resistance"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "TrfA locus from RK2 coding for two proteins P285 and P382 enabling an increase in the replication rate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "ori
264. .2603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "rice actin intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "nopaline synthetase terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "NPT III gene coding for neomycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "rice actin
685. .6858
 1699 A; 1694 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .6626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .5150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "T-DNA right border"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ColE1"
                                                                                                                                                                                                                                        and for preparing transgenic
                                                                                                                                                                                                                                                                                                                                      SA
  1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter"
  ດ
  1553 T; 0 U; 0 Other;
                                                                                                                                                                                                                                           plants.
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Query Match

13.8%:

Score 163;

BB

4

Length 6865;

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RESULT 13
AAF80295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  á
Best Local Similarity Matches 163; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of plasmid pMRT1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF80295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF80295 standard; DNA; 10003
                                  SgS
                                                                                                                                                                                 Sg
                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                          Sg
                                                                                                                                                                                                                                                                                                               Sas
                                                                                                                                                                                                                                                                                                                                      rep_origin
                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2001
       terminator
                                                                                       promoter
                                                                                                                  promoter
                                                                                                                                             intron
                                                                                                                                                                                                           terminator
                                                                                                                                                                                                                                                                                                                                                                   rep_origin
                                                            intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6383 TTTTATAATAGTAGAAAAGAGTAAATTTCACTTTGGGCCACCTTTTATTACCGATATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTITATACCACCITTIAACIGATGITTICACITTIGACCAGGIAATCITACCITTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTITATACCACCITITAACIGATGITITICACITITIGACCAGGIAATCITACCITIGITIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTATAATAGTAGAAAAGAGTAAATTTCACTTTGGGCCACCTTTTATTATCCGATATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                           /*rag= b
/note= "ori ColE1"
1264. .2603
     /note= "GUS gene coding for beta glucuronidase" 9497. .9823
                                                                                                                                                                                                                                               and P382 enabling
                                /note= "rice;
7688. .9496
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                    /note= "T-DNA
                                                                                       note= "rice actin
6672. .7107
                                                                                                                                                                                                          1272. .4559
                                                                                                                                                                                                                                                                                  hosphotransferase
                                                                                                                                                                                                                                                                                                                                                  note= "ori RK2"
                                                                                                                                                     cetyltransferase
                                                                                                                                                               note= "Bar
                                                                                                                                                                                         note= "nopaline
                                                                                                                                                                                                                                               note= "TrfA locus from RK2 coding for two proteins P285
nd P382 enabling an increase in the replication rate"
                                                                                                                                                                                                                                                                         604. .4098
                                                                                                                                                                                                                                                                                   note= "NPT III gene coding for neomycin
hosphotransferase and kanamycin resistar
                                                                                                                           note= "rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                         .1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. No.
                                                            e= "wheat
. .7687
                                                                                                                 .6638
                                                                                                                                                                                 .5169
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                                                                                                                                                                gene
                                           actin
                                                                                                                            actin intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                     left border"
                                                                      high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                              coding for pnospurate resistance"
                                                                                                                                                                                         synthetase terminator"
                                                                      molecular
                                                                                                promoter"
                                           intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1e-70;
                                                                      weight
                                                                                                                                                                                                                                                                                   resistance"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                      glutenin promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282
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RESULT 14
ADP83768
ID ADP83
XX ADP83
XX ADP83
XX DP83
XX DP83
XX DP83
XX DF Bents
XX W ds; k
XX Agroe
OS Chime
OS Unidd
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (especially a plant cell). The vector consists of at most one origin of replication (ori), at most one sequence encoding a selection agent and a trfA locus encoding a protein that increases the level of plasmid replication. The vector particularly contains an RK2 ori, especially oriV from pRK2 of Escherichia coli with a broad host range, an antibiotic resistance gene (especially nptIII conferring resistance to kanamycin in bacteria) and a trfA locus from pRK2 encoding the proteins P285 and P382. The vectors are used to prepare transgenic plants and transformed host cells for production of a heterologous proteins, e.g. insulin, interferon, lipase, blood proteins and anti-inflammatory agents. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New vector free from non-essential elements, useful for transforming cells for protein production and for preparing transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
             Agrostis vinealis. Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 163-166; 180pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAR-2001
                                                        glyphosate
                                                                                                 Bentgrass event ASR-368 3' transgene/genomic chimeric DNA SEQ
                                                                                                                               09-SEP-2004
                                                                                                                                                                                    ADP83768 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence represents a plasmid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erements essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The specification describes a synthetic vector containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MERI-) MERISTEM THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FR2798139-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                     bentgrass;
                                                                                                                                                                                                                                                            6522
                                                                                                                                                                                                                                                                                                                  6462
                                                                                                                                                                                                                                                                                                                                                                           6402
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                                                                                                                                                                                                                                                                                      283
                                                                                                                                                                                                                                                                                                                                               223
                                                                                                                                                                                                                                                                                                                                                                                                      163
                                                                                                                                                                                                                                                                                                                                                                                                                                  163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۲
                                                                                                                                                                                                                                                                                                                   ACTITATACCACCITTTAACTGATGTTTTCACTTTTGACCAGGTAATCTTACCTTTGTTT
                                                                                                                                                                                                                                                                                                                                                                          TTTTATAATAGTAGAAAAGAGTAAATTTCACTTTGGGCCACCTTTTATTATCCGATATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10003 BP; 2476 A; 2470 C; 2729 G;
                                                                                                                                                                                                                                                           ACTTTATACCACCTTTTAACTGATGTTTTCACTTTTGACCAGGTAATCTTACCTTTGTTT
                                                                                                                                                                                                                                                                                                                                                                                            TTTTATAATAGTAGAAAAGAGTAAATTTCACTTTGGGCCACCTTTTATTACCGATATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comeau D;
                                                        herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                 13.8%; So ilarity 100.0%; I Conservative 0;
                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99FR-00011112
                                                                      ASR-368;
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9823...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= n
/note= "T-DNA right border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for its functionality and transgenesis of a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "nopaline synthetase terminator"
.9996
                                                                                                                                                                                        474
                                                                     turfgrass
                                                                                                                                                                                        ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 163;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SA
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                      stand;
                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 10003;
                                                                      herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2328 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 U; 0 Other;
                                                                                                                                                                                                                                                                                       325
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                                                                                                    NO:4.
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11-JUN-2001; 2001US-0297406P 05-JUN-2002; 2002WO-US017853.

(MONS ) MONSANTO TECHNOLOGY LLC.

WO2002100163-A2

Agrobacterium tumefaciens

Insect

resistance; MON15985

16-APR-2003

(first

entry)

209 120

6 149

tumefaciens

DNA used in the exemplification of the

event; plant breeding;

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RESULT 15
AAD51491
ID AAD51
XX AAD51
XX AAD51
XX AAD51
XX Insec
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                   The invention relates to insect resistant cotton plants, tissues and seeds that include the MON15985 event. The methods and compositions of the invention are useful in the field of plant molecular biology, in particular plant insect protection and plant breeding. The MON15985 event confers resistance to Lepidopteran insect damage. The present sequence is A. tumefaciens DNA used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                       Sequence 349 BP; 101 A; 68 C; 74 G; 106 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 47; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insect resistant cotton plants, tissues and seeds that include the MON15985 event, useful in plant insect protection and plant breeding.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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163 163 147	169	171	1183 305 202	Score 1183	
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Sequence 13, Appl Sequence 21, Appl Sequence 23, Appl	Sequence 1, Appli Sequence 5, Appli	Sequence 49, Appl Sequence 44, Appl	Sequence 8, Appli Sequence 58081, A Sequence 27, Appl	Description Sequence 8, Appli	

45	44	43	42	41	40	39	38	37	36	ω 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
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11.3	11.3	11.3	11.3	11.3	11.3	11.3		11.5	11.5	11.5	11.5		11.5	11.6	11.6	11.6	11.6			11.6	11.6		11.6	11.8	11.8	12.2	12.4		12.4	12.4	12.4	12.4	12.4
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## ALIGNMENTS

US-09-872-051-8

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Sequence 8, Application US/09872051
Patent No. US20020013960A1
GENERAL INFORMATION:
APPLICANT: Monsanto Co
APPLICANT: Hironaka, Catherine
APPLICANT: Heck, Gregory
APPLICANT: Heck, Gregory
APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for I
TITLE OF INVENTION: Thereof
FILE REFERENCE: 38-21(52258)B
CUCRENT APPLICATION NUMBER: US/09/872,051
CUCRENT APPLICATION NUMBER: 60/213,567
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR APPLICATION NUMBER: 60/240,014
PRIOR PILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 16
SOPTWARE: PatentIn version 3.0
SQ ID NO 8
LENGTH: 1193
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: SOURCE
LOCATION: (1)..(1183)
OTHER INFORMATION: 1-164 Agrobacterium tumefaciens nos 3' terminator
OTHER INFORMATION: 165-381 Construct vector DNA
OTHER INFORMATION: 687-1183 Zea maize genomic DNA
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          GGTCGCGGGGCCCGATTTTTATAGCCTGGGCGAGGACGAGCTTGGCCGAACCGATCCAGA
                                                         TCTCTGTCTTCAACTTGCGCCGGCAGTCTGCTAGACCCAGGGGATGCTGTGTGGAGGAGA
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APPLICANT: Behr, Carl
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ACTGATGTTTTCACTTTTGACCAGGTAATCTTACCTTTGTTTTATTTTTGGACTATCCCGA

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PRIOR APPLICATION NUMBER: US/09/872,051
PRIOR FILING DATE: 2001-06-01
PRIOR PPLICATION NUMBER: 60/213,567
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR FILING DATE: 2000-10-13
PRIOR PPLICATION NUMBER: 60/240,014
PRIOR FILING DATE: 2000-10-13
PRIOR PPLICATION NUMBER: 60/240,014
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 2000-10-13
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
FEATURE:
LOCATION: (1)..(1183)
LOCATION: 1183)
LOCATION: 1-164 Agrobacterium tumefaciens nos
OTHER INFORMATION: 165-381 construct vector DNA
OTHER INFORMATION: 382-686 Zea maize plastid genes, rp
OTHER INFORMATION: 687-1183 Zea maize genomic DNA
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Best Local Similarity 100.0%; F
Matches 1183; Conservative 0;
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APPLICANT: Heck, Gregory
APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603)
TITLE OF INVENTION: Thereof
FILE REPERENCE: 38-21(52258)B
CURRENT APPLICATION NUMBER: US/10/790,430
CURRENT FILING DATE: 2004-03-01
CURRENT FILING DATE: 2004-03-01
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                            GAGTAAATTTCACTTTGGGCCACCTTTTATTACCGATATTTTACTTTATACCACCTTTTA
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RESULT 3
US-10-425-115-58081/c
; Sequence 58081, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
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                                                                                                                                              CAGCGCCCAGAGAAAAAAAAAGAAAGGAAGGCGCGAGATGATG
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GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: phosphonate Metabolizing Pl.
FILE REFERENCE: 38-21(15303)
CURRENT APPLICATION NUMBER: US/10/213,791
CURRENT APPLICATION NUMBER: US/9/441,340
PRIOR APPLICATION NUMBER: US/9/441,340
PRIOR APPLICATION NUMBER: 60/108,763
PRIOR APPLICATION NUMBER: 60/108,763
PRIOR APPLICATION NUMBER: 60/108,763
PRIOR FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 2378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Nucleic Acid Molecul
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,11
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 58081
LENGTH: 6683
TYPE: DNA
ORGANISM: Zea may8
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US-10-213-791-27/c
; Sequence 27, Application
; Publication No. US2003010
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Best Local Similarity
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           PEATURE:
NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                         OTHER INFORMATION: Description of Artificial Sequence:expression OTHER INFORMATION: cassette comprising a plant promoter linked to OTHER INFORMATION: intron, a sequence encoding an AMPA acetyl OTHER INFORMATION: transferase, and a termination sequence
                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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APPLICANT: Warner, Simon
APPLICANT: Andrews, Christopher
APPLICANT: Bachoo, Sarvinder
APPLICANT: Bichoo, Sarvinder
APPLICANT: Pickerill, Andrew
TITLE OF INVENTION: Herbicide Resistant Plants
FILE REFERENCE: 50490/UST
CURRENT APPLICATION NUMBER: US/10/012,070A
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: PCT/GB00/01573
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 57
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US-10-012-070A-49/c
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Best Local S
Matches 202
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Best Local Similarity
Matches 171; Conserv
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SEQ ID NO 49
LENGTH: 1501
TYPE: DNA
ORGANISM: Oryza sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49, Application US/10012070A
Publication No. US20030077801A1
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LOCATION: (1668)..(2099)
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LOCATION: (1440)..(1667)
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les 202; Conserv
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                                                                                                   ACTTTATACCACCTTTTAACTGATGTTTTCACTTTTGACCAGGTAATCTTACCTTTGTTT 282
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                              TTTTATAATAGTAGAAAAGAGTAAATTTCACTTTGGGCCACCTTTTATTACCGATATTTT
                                                                                                                                                                       TTTTATAATAGTAGAAAAGAGTAAATTTCACTTTGGGCCACCTTTTATTACCGATATTTT
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                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                      14.5%; Score 171; DB 14;
100.0%; Pred. No. 8.2e-79;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                          DB 14; Length 1501;
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                                                                  801
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; LENGTH: 2480
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: transcriptional unit comprising promoter, coding sequence for contract information transcription factor of SEQ ID NO:2 and terminator elements
US-10-678-588A-1
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US-10-012-013-44/c
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APPLICANT: Warner, Simon
APPLICANT: Warner, Simon
APPLICANT: Bachoo, Satvinder
APPLICANT: Bachoo, Satvinder
APPLICANT: Pickerill, Andrew
TITLE OF INVENTION: Herbicide Resistant Plants
FILE REFERENCE: 50450/UST
CURRENT APPLICATION NUMBER: US/10/012,013
CURRENT FILING DATE: 2001-10-29
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                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/678,588A CURRENT FILING DATE: 2003-10-02 PRIOR APPLICATION NUMBER: US 60/415,758 PRIOR FILING DATE: 2002-10-02 PRIOR APPLICATION NUMBER: US 60/425,157 PRIOR APPLICATION NUMBER: US 60/463,787 PRIOR FILING DATE: 2003-04-11 PRIOR FILING DATE: 2003-04-11
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                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.2 SEQ ID NO 1
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Publication No.
Query Match 14.3%; Score 169; DB 19; Length 2480; Best Local Similarity 100.0%; Pred. No. 9.2e-78; Matches 169; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wu, Jingrui TITLE OF INVENTION: Water-Deficit-TolerantTransgenic FILE REFERENCE: 38-21(52578)C
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 10
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TYPE: DNA
ORGANISM: Oryza sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 14.5%; Score 171; DB 14; Local Similarity 100.0%; Pred. No. 8.2e-79; hes 171; Conservative 0; Mismatches 0;
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Gaps

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APPLICANT: Frank Michiels et al.
TITLE OF INVENTION: Improved Barstar Gene
FILE REFERENCE: 2428-0108P
CURRENT APPLICATION NUMBER: US/09/970,921
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
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US-09-970-921-5/c
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WE-09-645-064-13
US-09-645-064-13
; Sequence 13, Application US/09845064
; Publication No. US20030175976A1
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Patent No. US20020133845A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                        Matches
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LOCATION: (3677)..(4003)
OTHER INFORMATION: label =
OTHER INFORMATION: end of
OTHER INFORMATION: T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (3399)..(3404)
OTHER INFORMATION: label =
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (3401)..(3676)
OTHER INFORMATION: label =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (1995)..(3400)
OTHER INFORMATION: label = PRAC1, "promoter region of rice
OTHER INFORMATION: - contains an intron in the leader"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: other nucleic OTHER INFORMATION: acid, "plasmid pMV71"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 4032
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ilarity 100.0%;
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; Pred. No. 3.1e-77
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "region containing 3' untranslated
ne synthase gene of Agrobacterium
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                                                                                                                                                                                                                                                                                                                                     Length 4032;
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; OTHER INFORMATION: T-DNA US-09-845-064-13
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APPLICANT: MERISTEM THERAPEUTICS
APPLICANT: MERISTEM THERAPEUTICS
TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS
TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR
TITLE OF INVENTION: METHODS OF PRODUCTION
FILE REFERENCE: SynVec1
CURRENT APPLICATION NUMBER: US/09/845,064
CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PATENTIA DOS: 57
SOFTWARE: PATENTIA B665
TYPE: DNA
ORGANISM: Artificial Sequence
  Query Match
Best Local S
Matches 163
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NAME/KEY: gene
LOCATION: (1264)..(2603)
OTHER INFORMATION: NPT III gene coding for neomycin
OTHER INFORMATION: phosphotransferase and kanamycin
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NAME/KEY: terminator
LOCATION: (4272)...(4559)
OTHER INFORMATION: No. U
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NAME/KEY: rep_origin
LOCATION: (1)..(654)
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LOCATION: (4575)..(5150)
OTHER INFORMATION: Bar gene coding for I
OTHER INFORMATION: acetyltransferase and
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LOCATION: (4106)...(4271)
OTHER INFORMATION: T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (2604)...(4098)
OTHER INFORMATION: TrfA locus from RK2 coding for two proteins, P285
OTHER INFORMATION: and P382, enabling the increase in the replication
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                                                                                                                           NAME/KEY: misc feature LOCATION: (6685)..(685)
                                                                                                                                                                                       NAME/KEY: misc feature LOCATION: (6626)..(668 OTHER INFORMATION: MCS
                                                                                                                                                                                                                                                                     NAME/KEY: promoter LOCATION: (5686)..(6626)
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: intron
LOCATION: (5174)..
OTHER INFORMATION:
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                                                                                                                                                                                                                                                      FEATURE:
    163; Conser
13.8%; Score 163; DB 10; ilarity 100.0%; Pred. No. 1.3e-74; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                 (6685)
                                                                                                                                                                                                                                                                                                                                                           Rice
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                                                                                                                                                                                           site
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                                           Length 6865;
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        Gaps
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163 TTTTATAATAGTAGAAAAGAGTAAATTTCACTTTGGGCCACCTTTTATTACCGATATTTT

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LENGTH: 10003
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CURRENT APPLICATION NUMBER: US/09/845,064
CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MERISTEM THERAPEUTICS
TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS,
TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID V
                                                                                                 NAME/KEY: gene
LOCATION: (4594)..(5169)
OTHER INFORMATION: Bar go
OTHER INFORMATION: acety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (2604)...(4998)
OTHER INFORMATION: TrEA locus from RK2 coding for two
OTHER INFORMATION: and P382, enabling the increase of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: gene
LOCATION: (1264)..(2603)
OTHER INFORMATION: NPT III gene coding
OTHER INFORMATION: phosphotransferase a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: rep_origin
LOCATION: (655)..(1263)
OTHER INFORMATION: Origin of replication ori ColEI
NAME/KEY: intron
LOCATION: (5170)..(5704)
OTHER INFORMATION: Rice
FEATURE:
                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (4559)..(4572)
OTHER_INFORMATION: MCS multiple
                                                                                                                                                                                                                                                                                      NAME/KEY: terminator
LOCATION: (4272)..(4559)
OTHER INFORMATION: No. US20030175976Alaline synthetase
                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (4106)..(4271)
OTHER INFORMATION: T-DNA
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LOCATION: (1)..(654)
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                     Rice Actin Intron
                                                                                                 Bar gene coding for phosphinothricine acetyltransferase and glufosinate resistance
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                                                                                                                                                                                                                                                                                                                                                     Sequence 23, Ap
Publication No.
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Matches 163;
SEQ ID NO 23
LENGTH: 349
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                                                                                                      APPLICANT: Doherty, Sean C.
APPLICANT: Roberts, James K.
APPLICANT: Shappley, Zachary W.
APPLICANT: Shappley, Zachary W.
TITLE OF INVENTION: Cotton Event 15985 and Compositions and TITLE OF INVENTION: Thereof
FILE REFERENCE: 11899.0232.PCUS00
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: US 60/297406
PRIOR APPLICATION NUMBER: US 60/297406
PRIOR FILING DATE: 2001-06-11
                                                  PRIOR APPLICATION NUMBER: PCT/US 02/17853
PRIOR FILING DATE: 2002-06-05
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                               APPLICANT: Monsanto, Technology APPLICANT: Huber, Scott A
                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (9823)..(9996)
OTHER INFORMATION: T-DNA right border
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: intron
LOCATION: (7169)..(7687)
OTHER INFORMATION: Rice Actin
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LOCATION: (6646)..(6672)
OTHER INFORMATION: MCS multiple cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: terminator
LOCATION: (9497)..(9823)
OTHER INFORMATION: No. U
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LOCATION: (5705) ..(6638)
OTHER INFORMATION: Rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
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OTHER INFORMATION: High Molecular Weight Glutenin promoter from wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (7107)..(716
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                                      PatentIn version 3.2
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(7688)..(9496)
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to. US20040250317A1
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; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-480-223A-23
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US-10-480-223A-12
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SEQ ID NO 12
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Best Local
                                                                                                                                                                               Matches
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CURRENT APPLICATION NUMBER: US/10/480,223A.
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: US 60/297406
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: PCT/US 02/17853
PRIOR FILING DATE: 2002-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Doherty, Sean C.
APPLICANT: Roberts, James K.
APPLICANT: Shappley, Zachary W.
TITLE OF INVENTION: Cotton Event 15985 and Compositions and Methods for Detection
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Monsanto, Technology LLC APPLICANT: Huber, Scott A APPLICANT: Doherty, Sean C.
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                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)..(349)
OTHER_INFORMATION: 3' end insert sequence
                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature LOCATION: (350)..(673) OTHER INFORMATION: 3'
                                                                                                                                                                                                                                                                 LOCATION: (674)...(1360)
OTHER INFORMATION: 3' end Gossypium hirsutum chromosomal sequence
                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature 
LOCATION: (674)..(1360
                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1360
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les 147; Conserv
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   GTTACTAGATCGGGGATATCCCCGGGG 147
                                     GACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGC
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                                                                                                                                                                                 Conservative
                                                                                                                                                                               12.4%; Score 147; DB 18; 100.0%; Pred. No. 3.4e-66; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                             end
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US-10-232-665-13
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                                                                                                                                  Sequence 13, Application US/10232665
Publication No. US20030115630A1
GENERAL INFORMATION:
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LENGTH: 3754
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PRIOR APPLICATION NUMBER: US/09/377,466
PRIOR FILING DATE: 1999-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/10/232,665
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US/09/377,466
PRIOR FILING DATE: 1999-08-19
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CURRENT FILING DATE: 2002-08-29
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LOCATION: (3475)..(3730)
OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription
OTHER INFORMATION: termination and polyadenylation sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: CDS
LOCATION: (1490)..(3448)
OTHER INFORMATION: Cry3Bbl variant v11231
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OTHER INFORMATION: I-Zm.
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US-10-198-478-16
Sequence 16, Application US/10198478
Sequence 16, Application US/10198478
Sequence 16, Application US/10198478
Sequence 16, Application US/10198478
FULL CAPTION US20030188336A1
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Romano, Charles P.
TIFLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotox FILE REFERENCE: 38-21 (13547) B
CURRENT APPLICATION NUMBER: US/10/198,478
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/186, 002
PRIOR FILING DATE: 1998-11-04
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Best Local Similarity
Matches 147; Conserv
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SOPTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 4149
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KRY: terminator
LOCATION: (3871)...(4127)
OTHER INFORMATION: T-AGRETU.nos 3' t
OTHER INFORMATION: polyadenylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (1885)..(3843)
OTHER INFORMATION: Cry3Bb1 variant v11231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: transit_peptide
LOCATION: (1799)..(1885)
OTHER _INFORMATION: carboxy terminus TS-Zm.rbcS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: promoter
LOCATION: (25)..(640)
OTHER INFORMATION: P-CAMV.35S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
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LOCATION: (1636)..(1798)
OTHER INFORMATION: I-Zm.rbcS
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LOCATION: (1489)..(1635)
OTHER INFORMATION: amino terminal
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LOCATION: (669)..(1472)
OTHER INFORMATION: I-Zm.Hsp70
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; AMME/KEY: misc feature
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US-10-198-478-16
Search completed: February Job time: 1969.4 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: completely synthesized
                                                                      5842 GTTACTAGATCGGGGATATCCCCGGGG 5868
                                                                                                                                          5722 GACGTTATTTATGAGATGGGTTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGC 5781
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Abl09088 Drosophil
Adf59752 Human com
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Aac93637 Cat flea	Adn/0/25 Human den Ach77045 Human den	нитал	Human	Human	Human	Human		Ach90762 Human gen	Ach94209 Klebsiell	Aca35231 Prokaryot	Ach46396 Human int	Abv36267 Human pro	Aca44008 Proxaryor		Adi55601 Human pol	Aca55805 Zebratish	Abv36189 Human pro	Abs13933 Human gen	Human	Human	Human	Abv154/5 Human pro	AGG40/62 MULTING LE	· Adapto Kindao to

## ALIGNMENTS

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Zea mays.
Synthetic.
                                                                                                                                                                                                                                                   Probe; ss; rice actin 1 promoter; RA1; RA1 intron; chloroplast transit peptide gene; glyphosate resistance; corn; 5-enol-pyruvylshikimate-3-phosphate synthase; EPSPS; Hsp70 intron; transcriptional terminator; cauliflower mosaic virus 35S promoter; pV-ZMGT32; transgenic; nk603.
                                                                                                                                                                                                                                                                                                         Corn transgene junction probe #3.
                                                                                                                                                                                                                                                                                                                                             ABK15248;
                                                                                                                                                                                                                                                                                                                                                              ABK15248 standard; DNA; 18
                                                                                                                                  22-JUN-2000; 2000US-0213567P
13-OCT-2000; 2000US-0240014P
13-OCT-2000; 2000US-0241215P
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                                                                                                                  (MONS ) MONSANTO TECHNOLOGY LLC
                                                                                                                                                                                                                                                                                                                           (first entry)
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The invention relates to a DNA construct (I) comprising a first (F1) and a second (F2) expression cassette. F1 of the DNA construct, in operable

and

Novel DNA construct useful for producing a corn plant that tolerates application of glyphosate herbicide, comprises two transgene expression

WPI; 2002-165871/22.

Behr CF,

Hironaka C,

Heck GR,

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Claim 8; Page 3; 25pp; English

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RESULT 2
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  Behr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ds; rice actin 1 promoter; RA1; RA1 intron;
chloroplast transit peptide gene; glyphosate resistance; corn;
5-enol-pyruvylshikimate-3-phosphate synthase; EPSPS; Hsp70 intron;
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                                                     TECHNOLOGY LLC.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a DNA construct (I) comprising a first (F1) and a second (F2) expression cassette. F1 of the DNA construct, in operable linkage, has rice actin 1 (RA1) promoter, RA1 intron, chloroplast transit peptide gene (II), 9lyphosate tolerant 5-enol-pyruvylshikimate-3-phosphate synthase (FPSPS) gene (III), and transcriptional terminator (IV), and F2 has cauliflower mosaic virus 35S promoter, Hsp70 intron, (III), (III) and (IV). Also included are two DNA sequences from corn plant Pv-ZMGT32(nk603) of 498 or 1183bp, or primers and probes derived from them (used to detect transgene junction points). The construct is useful for producing a corn plant that tolerates application of 9lyphosate herbicide by transforming a corn cell with, selecting the corn cell into a fertile corn plant. The present sequence is the 1183bp amplicon consisting of the Agrobacteium transcriptional terminator sequence,
                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1183 BP; 295 A; 289 C; 280 G; 319 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       application of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-165871/22
                                                                                                                                                                                                          P-PSDB;
                                                                                                                                                                                                                                                                                                Drmanac
                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS66560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS66560 standard; cDNA; 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vector sequences and corn sequences
                                                                                                                                                                                                          2001-639362/73.
DB; ABG02373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              678 TGCTGTTCTGCTGACTTT 695
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                                                                                                                                                                                                                                                                                                RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     construct
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2000US-00649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                ņ
                                                                                                                                                                                                                                                                                                Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                   ΥŢ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1183;
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Claim 1; SEQ

ID NO 2364; 103pp; English

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RESULT 4
AAH14053
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Best Local S
Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1361 BP; 414 A; 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2001
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                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUL-2000; 2000EP-00116126
                                                                                                                                                                                                                                             WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                          Isogai T,
Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCTGTTCTGCTGACT 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTGTTCTGCTGACT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 99JP-00248036.
; 99JP-00300253.
; 2000JP-00118776.
; 2000JP-00183767.
; 2000JP-00241899.
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                                                                                                                                                                                                                                                                                                          Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:11181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                             Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313
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27;
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                                                                                                                                                                                                                                                                                                                 Saito K, Y
, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 U;
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                                                                                                                                                                                                                                                                                                                                                     Yamamoto
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Claim 8; SEQ ID NO 11181; 2537pp + Sequence Listing; English

Novel biallelic markers used to construct a high density disequilibrium map of the human genome.

Claim 9; Page 1852; 2745pp;

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1587 BP; 312 A; 416 C; 383
                                                                                                                                                                                      WPI; 2000-013267/01
                                                                                                                                                                                                                                                   Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                21-APR-1998;
23-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human biallelic marker upstream amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
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16; Conserv
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                                                                                                                                                                                                                                                       Blumenfeld
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98US-0109732P
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                                                                                                                                                                                                                                                          Chumakov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer SEQ ID NO:7605.
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RESULT 6
ABV19889/c
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XX ABV198
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Best Local S
Matches 15
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
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13-DEC-2000;
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N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing
                                                                                                                                                                                                                                                    prostate
for detec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate pharmacogenomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-)
                                                                                                                                                                                                                                                                                                                                                                 2001-662795/76.
                                                                                                                                                                                                                                                 isolated nucleic acid molecule associated with cancerous state ate cells and correlating with presence of prostate cancer, use etecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prostate
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2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
2000US-0255281P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                             3245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer; cytostatic; carcinogen; pharmacodyanamic
marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PREDICTIVE
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Pred. No
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                                                                                                                                                                                             English
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                                                                                                                                                                                                                                                                                tate of useful
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RESULT 7
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Query
Best I
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18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patien; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                      a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a thorapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cell carcinogenic potential of a compound; (g) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                              a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of a specification or its complement. (I) is useful for: (a) assessing
                                                                                                                                                                                                                         prostate cells and corr
for detecting presence
                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                           Schlegel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
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                                                                                                                                                          The invention relates a nucleotide sequence
                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                      Novel isolated
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16-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABV49652;
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                                                                                                                                                                                                 Page 9689; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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2000US-0207454P.
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                                                                                                                                                                                                                                        nucleic acid molecule associated with cancerous state and correlating with presence of prostate cancer, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression marker cDNA 49643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; cytostatic; carcinogen;
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                                                                                                                                                                                                                            of prostate cancer,
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                                                                                                                                                         isolated nucleic acid in Tables 1-9 (ABV000)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
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                                                                                                                                                                                                                            of prostate
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Sequence

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116 G;

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RESULT 8
ABL09089
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                               RESULT 9
ADE59493/c
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Best Local
                                                                                                                            Matches
                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                       capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABI16176-ABH30511), expressed DNA sequences (ABI01840-ABH16175) and the encoded proteins (ABB5737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster expressed polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL09089
                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 21749; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL09089 standard; cDNA; 715
ADE59493;
                    ADE59493 standard; DNA; 2280
                                                                                                                                                                       Sequence
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                                                                                                                                                                       715
                                                                                          TGCTGTTCTGCTGAC 15
                                                                               TECTETTCTECTEAC 102
                                                                                                                                                                                              at
                                                                                                                                                                                                                                                                                                                                                                                                                               Adams M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                           Conservative
                                                                                                                                                                       BP;
                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene;
                                                                                                                                                                       151 A; 192 C; 202 G; 170 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                     83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                , dwa
                                                                                                                                                                                                                                                                                                                                                          detection reagent for detecting 1000 for elucidating cell signaling and ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No.
                                                                                                                                     Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                Myers
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                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
                                                                                                                                       91;
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                                                                                                                             Gaps
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construction of a polynucleotide sequence which is differentially corporated to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound to small molecule that regulates the cativity in an animal of one or more of the polypeptides given in the generation, a method for identifying a compound useful in treating compain and a pharmaceutical composition comprising the one or more completed to the regulates the compound a pharmaceutical composition comprising the one or more conjugated to their antibodies. The polynucleotide or the compound that conjugate in (e.g. spinal segmental nerve injury (Chung), chronic constriction conjugated in a segment of the polynucleotide or the greating conjugated in a segment of the polynucleotide or the greating conjugated in a segment of the polynucleotide or the greating conjugated in the conjugated in the conjugated in the conjugated conjugated in the polynucleotide or the greating conjugated in the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New composition comprising preparing a medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Woolf C, D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         spinal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or human polynucleotides or a polynucleotide which represents a fraderivative or allelic variation of the nucleic acid sequence. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention discloses a composition comprising two or more isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENBANK;
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(FARB )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003016475-A2
ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds; gene; pain; neuronal tissue; gene therapy;
segmental nerve injury; chronic constriction injury; CCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEN HOSPITAL
BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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741

TGTTCTGCTGACTTT 727 TGTTCTGCTGACTTT 18

4 15;

Matches Query Match Best Local

Similarity

83.3%; 100.0%;

Score 15; Pred. No.

DB 10; 97;

Length 2280;

Conservative

0

Mismatches No.

0

0

Gaps

0

Sequence 2280 BP; 680 A; 358 C;

392 G; 850 T;

0 U; 0 Other;

₽P

0

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RESULT 10
ADE59491/c
ID ADE59491 standard; DNA; 2280
                         con human polymucleotides or a polymucleotide which represents a fragment, comprising the variation of the nucleic acid sequence. Also calaimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence (which is differentially regulated in an animal subjected to pain and a ckit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence ct that is differentially expressed in neuronal tissue of a first animal cubic telescope in an animal subjected to pain, a method for identifying an agent compound that regulates the activity of one or more of the regulates compound that regulates the activity of one or more of the composition, a compound that regulates the activity of one or more of the regulates the cativity in an animal of one or more of the polypeptides given in the composition and a pharmaceutical composition comprising the one or more completed to pain and a pharmaceutical composition comprising the one or more complypeptides or their antibodies. The polymucleotide or the compound that composition and a pharmaceutical composition comprising the one or more complypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating capain (e.g. spinal segmental nerve injury (CNI)) in an animal (e.g. gene therapy). The sequence presented is a human DNA (shown in Table 2 of the specification) which encodes one of the polypeptides of the invention contained in electronic form part of the printed specification, but was cotained in electronic form part of the printed specification, but was cotained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human;
spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003016475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene AK001865,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention discloses a composition comprising two or more isolated rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003-268312/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) GEN HOSPITAL CORP.
) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ds; gene; pain; neuronal tissue; gene therapy;
segmental nerve injury; chronic constriction injury; CCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Query Match Best Local Similarity

83.3%;

Score 15; Pred. No.

Length 2280 U; 0 Other;

Sequence

2280

B₽; 680

A; 358 C; 392 G;

850 DB 97; 10; T; 0

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RESULT 11
AAS30480
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                                                                                        14-AUG-2000;
14-AUG-2000;
                                                                                                                 14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
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14-AUG-2000;
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07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; nootropic; neuroprotective; cytostatic; antiparkinsonian;
antianaemic; dermatological; immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding novel prostate gland antigen, Seq ID No
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26-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                         2000US-0220964P.
2000US-0224519P.
2000US-0225213P.
2000US-0225214P.
2000US-022526P.
2000US-022526P.
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2000US-022526P.
2000US-022575P.
2000US-0225759P.
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                                                                                                                              The invention relates to novel isolated prostate gland related nucleic cc acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis. CC prognosis, prevention, and/or treatment of diseases and/or disorders of the prostate such as acute non-bacterial prostatitis, chronic non-cc bacterial prostatitis, acute bacterial prostatitis, prostatodystonia, prostatosis, granulomatous prostatitis, malacoplakia, benign prostatic cc hypertrophy or hyperplasia, and prostate neoplastic disorders, including cc adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and cc squamous cell carcinomas. (I), (II) and antibody to (II) are useful for diagnosing and treating reproductive system disorders (Paget's disease), cc autoimmune disorders (systemic lupus erythematosus, rheumatoid cc arthritis), blood-related disorders (sickle cell anaemia), hyperproliferative disorders, urinary system disorders (Paget's disease), cc (glomerulonephritis), cardiovascular disorders (arrhythmias), respiratory cellomerulonephritis), cardiovascular disorders (arrhythmias), respiratory cellomerulonephritis), cardiovascular disorders (arrhythmias), respiratory cellomerulonephritis), cardiovascular disorders, neural activity and cellomerulonephritis), cardiovascular disorders, neural activity and cellomerulonephritis), cardiovascular disorders (arrhythmias), respiratory disorders (Alzheimer's disease and Parkinson's disease), pastrointestinal disorders (inflamatory disorders), liver disorders (biliary liver cirrhosis), pancreatic and gall bladder disorders (biliary liver cirrhosis), cuseful to prevent skin aging, for preventing hair loss, to maintain corgans before transplantation, and as food additive or preservative.
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Matches 15
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01-DEC-2000;
01-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated prostate gland related polypeptide useful for diagnosis and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia
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                    TGTTCTGCTGACTTT
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01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 05-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 14-SEP-2000 11-SEP-2000 11-SEP-2000 21-SEP-2000 22-SEP-2000 22-SEP-2000 23-SEP-2000 23-SEP-2000 23-SEP-2000 23-SEP-2000 23-SEP-2000 23-SEP-2000 20-OCT-2000 20-OC

2000US-022934PP.
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2000US-022950SP.
2000US-023124SP.
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05-DEC-2000; 05-DEC-2000; 06-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000;

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding a reproductive system antigen used in preventing, treating or ameliorating a medical condition.
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11-DEC-2000;
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  New isolated nucleic acid genes from Drosophila and
                                                                   WPI; 2001-656860/75.
P-PSDB; ABB64985.
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2000US-0251030P.
2000US-025671998P.
2000US-0256719P.
2000US-0251479P.
2000US-0251856P.
2000US-0251869P.
2000US-0251869P.
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2000US-00614150.
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                                                                                                                                        PWD,
detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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Pred. No.
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RESULT .14
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The present invention describes isolated polynucleotide sequences (I), which encode polypeptides (II) with biological activity. Also described:
(1) a vector comprising (I); (2) an expression vector comprising (I); (3)
a host cell genetically engineered to comprise (I) which is operatively associated with a regulatory sequence that modulates expression of (I) in the host cell; (4) a polypeptide (II) encoded by (I); (5) a composition comprising the polypeptide of (4) and a carrier; (6) an antibody directed against the polypeptide of (4); (7) detecting (I) or the polypeptide of (4) in a sample; (8) identifying a compound that binds to the polypeptide of (4); (9) producing the polypeptide of (4); and (10) a collection of
                                                                                                                                                                                                               primers,
of protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 21746; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biological activity; genetic engineering; hybridisation probe; oligomer;
primer; chromosome mapping; gene mapping; recombinant protein production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human contig polynucleotide sequence SEQ ID NO:2119.
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                                                                                                                                                                                Example 2; SEQ ID NO 2119; 571pp; English.
                                                                                                                                                                                                            New polynucleotides, useful as hybridization probes, oligomers primers, for chromosome or gene mapping, for the recombinant professions, and for generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001; 2001US-0311261P
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DB; ADF60204.
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15; Conserv
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100.0%; Pr
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Pred. No.
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RESULT 15
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Best Local (
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18-APR-2000
19-MAY 2000
07-JUN-2000
30-JUN-2000
30-JUN-2000
07-JUL-2000
11-JUL-2000
11-JUL-2000
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14-JUL-2000
14-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynucleotides comprising at least one of the polynucleotide sequences (I). The polynucleotides (I) can be used as hybridisation probes, oligomers or primers, for chromosome or gene mapping, for the recombinant production of proteins, and for generating antisense DNA or RNA. The present sequence represents a human contrig polynucleotide sequence, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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7-MAR-2000;
3-APR-2000;
9-MAY-2000;
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TGTTCTGCTGACTTT
 2000US-011865P.
2000US-018664P.
2000US-0186350P.
2000US-0199076P.
2000US-0199076P.
2000US-029515P.
2000US-021647P.
2000US-021647P.
2000US-021647P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
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2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-0227566P.
2000US-02252767P.
2000US-0225759P.
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ilarity 100.0%;
Conservative
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Pred. No.
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1e+02;
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 23 AUG 2000
23 - AUG 2000
01 - SEP 2000
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06 - SEP 2000
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03 - SEP 2000
04 - SEP 2000
05 - SEP 2000
06 - NOV 2000
07 - SEP 2000
08 - NOV 2000
09 - NOV 2000
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 2000US-0246525P.
2000US-0246526P.
2000US-0246528P.
2000US-0246532P.
2000US-0246610P.
2000US-0246611P.
2000US-0246613P.
2000US-0249208P.
2000US-0249209P.
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2000US-0244617P.

2000US-0246475P.

2000US-0246476P.

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2000US-0246478P.

2000US-0246523P.

2000US-0246523P.
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2000US-0237037P.
2000US-0237039P.
2000US-0237039P.
2000US-023993P.
2000US-0239937P.
2000US-0249260P.
2000US-0241785P.
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2000US-0234997P.
2000US-0234998P.
2000US-0235484P.
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2000US-0241787P.
2000US-0241808P.
2000US-0241809P.
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17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

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                                                                                                                                                                 AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) camino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) cyroteins and polynucleotides may be used in the prevention, diagnosis and creatent of diseases associated with inappropriate (I) expression. For cerample, they may be used to treat disporders associated with decreased cexpression by rectifying mutations or deletions in a patient's genome created that affect the activity of (I) by expressing inactive proteins or to complement the patients own production of (I). Additionally, (I) complement the patients own production of (I). Additionally, (I) concludes may be used to produce the secreted (I), by inserting the collic acids into a host cell and culturing the cell to express the complement immune/haematopoietic-related diseases, especially concers and cancer metastases of haematopoietic antigen genomic concers and cancer metastases of haematopoietic antigen genomic concers from the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
                                                                  Query Match
Best Local S
Matches 15
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01-DEC-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 41014; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-483426/52.
                                                                                                                                         Sequence 41335 BP; 9383 A; 10738 C; 10251 G; 10957 T; 0 U; 6 Other;
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34054 GCTGTTCTGCTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA, Barash SC,
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                                                                                       Similarity
                    GCTGTTCTGCTGACT 16
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2000US-0249211P.
2000US-0249211P.
2000US-0249211P.
2000US-0249211P.
2000US-0249211P.
2000US-0249211P.
2000US-024921P.
2000US-024921P.
2000US-024924P.
2000US-024924P.
2000US-024924P.
2000US-0249265P.
2000US-0249265P.
2000US-0249269P.
2000US-0249269P.
2000US-0259300P.
2000US-025930P.
2000US-0251988P.
2000US-0251866P.
2000US-0251866P.
2000US-0251989P.
                                                                  Conservative
                                                                                     83.3%; Score 15; DB 4; L
100.0%; Pred. No. 1.1e+02;
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34068
                                                                    0;
                                                                      Mismatches
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                                                                                                        Length 41335;
                                                                        Indels
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Search completed: February 10, 2005, 13:44:11 Job time: 21.6055 secs

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RESULT 2 US-09-441-340-27/c Ś

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APPLICANT: BATTY, Gerard F.
TITLE OF INVENTION: Phosphonate Metabolizing Plants
FILE REFERENCE: 38-21(1303)
CURRENT APPLICATION UNWHER: US/09/441,340
CURRENT FILING DATE: 1999-11-16
EARLIER APPLICATION NUMBER: 60/108,763
EARLIER FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 27
LENGTH: 2378
TYPE: DNA
                 Sequence 5, Application US/09068101
Patent No. 6372960.
GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Improved Barstar Gene
FILE REFERENCE: 2121-139P
CURRENT APPLICATION NUMBER: US/09/068,101
CURRENT FILING DATE: 1996-08-26
EARLIER APPLICATION NUMBER: EP 96202446.9
EARLIER APPLICATION NUMBER: EP 96202446.9
EARLIER FILING DATE: 1996-09-03
NUMBER OF SEQ ID NOS: 10
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GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE: FEATURE: OTHER INFORMATION: Description of Artificial Sequence:expression OTHER INFORMATION: cassette comprising a plant promoter linked to OTHER INFORMATION: intron, a sequence encoding an AMPA acetyl OTHER INFORMATION: transferase, and a termination sequence
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (1668)..(2099)
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(966)..(1423)
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100.0%; Pred. No. 2.5e-89;
vative 0; Mismatches 0;
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (4355)..(4
; OTHER INFORMATION: "
US-09-186-002-15
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US-09-186-002-15
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US-09-186-002-13
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APPLICANT: Corbin, David R.
APPLICANT: Romano, Charles P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, App....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 15
                                            APPLICANT: Corbin, David R.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Method for Transforming Plants to Express
TITLE OF INVENTION: delta-Endocoxins
FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
CURRENT APPLICATION NUMBER: US/09/186,002B
CURRENT FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
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Best Local Similarity
                                                                                                                                                                                                                           Sequence 13, Applia Patent No. 6489542
                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Improved Method for Transforming Plants to TITLE OF INVENTION: delta-Endotoxins FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002 CURRENT APPLICATION NUMBER: US/09/186,002B CURRENT FILING DATE: 1998-11-04 NUMBER OF SEQ ID NOS: 18
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NAME/KEY: unsure
LOCATION: (3660)..(3773)
OTHER INFORMATION: "n" =
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TYPE: DNA
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
               LENGTH: 10339
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                               3025
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2965 GACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGC 3024
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Pred. No. 2.9e-62;
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                                                               ; LOCATION: (2114)..(2369)
US-09-441-340-27
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Best Local Similarity
Matches 147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 2378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6448476
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 38-21(15303)
CURRENT APPLICATION NUMBER: US/09/441,340
CURRENT FILING DATE: 1999-11-16
EARLIER APPLICATION NUMBER: 60/108,763
EARLIER FILING DATE: 1998-11-17
               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Phosphonate Metabolizing Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (4382)..(4434)
OTHER INFORMATION: "n" =
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LOCATION: (3687)..(3760)
OTHER INFORMATION: "n"=g,
                                                                                                                                                FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                              FEATURE:
NAME/KEY: terminator
                                                                                                                                                                                NAME/KEY: transit_peptide LOCATION: (1440)..(1667)
                                                                                                                                                                                                                 FEATURE:
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                                                                                                                              LOCATION: (1668)..(2099)
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ilarity 100.0%;
Conservative
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               11.8%; Score 140; DB 3; 100.0%; Pred. No. 8.5e-59;
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Pred. No. 2.9e-62;
0; Mismatches 0;
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APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Phosphonate Metabolizing Plants
FILE REFERENCE: 38-21(15303)
CURRENT APPLICATION NUMBER: US/09/441,340
CURRENT FILING DATE: 1999-11-16
CURRENT FILING DATE: 1999-11-16
EARLIER APPLICATION NUMBER: 60/108,763
EARLIER FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 32
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 31
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Sequence 31, App-
No. 6448476
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US-09-441-340-23

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: transit_peptide LOCATION: (1498)..(1725)
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LOCATION: (17)
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US-09-098-219B-5
                                                                                                                                                                                                                                                                                            ; Sequence 5, Application US/09098219B ; Patent No. 6441277
                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Barry, Gerard

APPLICANT: Cheikh, No. 64412

APPLICANT: Kishore, Ganesh

TITLE OF INVENTION: Expressi

TITLE OF INVENTION: Aldolase
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                COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                     NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS:
                                                                                                                                          STREET:
                                                                                                                                                          ADDRESSEE:
                                                                                                                             Houston
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E: Arnold White & Durkee P.O. Box 4433

Barry, Gerard Cheikh, No. 6441277dine

Expression of Fructose 1,6 Bisphosphate Aldolase in Transgenic Plants

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APPLICANT: BAITY, Gerard F.
TITLE OF INVENTION: Phosphonate Metabolizing Pl.
FILE REFERENCE: 38-21(15303)
FILE REPERENCE: 38-21(15303)
CURRENT APPLICATION UNMBER: US/09/441,340
CURRENT FILING DATE: 1999-11-16
CURRENT FILING DATE: 1999-11-17
EARLIER APPLICATION NUMBER: 60/108,763
EARLIER FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID 00 23
                                                                                                                                                                                                                                                                                                             ; LOCATION: (1350)..(1605)
US-09-441-340-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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LOCATION: (893)..(1324)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: transit_peptide
LOCATION: (627)..(892)
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                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: terminator
                                                                                                                                                                                                                                      Local Similarity 100.0%;
les 137; Conservative (
                                                                            1596 GTTACTAGATCGGGGAT 1612
                                     121 GTTACTAGATCGGGGAT 137
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Minimum
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18
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Copyright (c) 1993 - 2005 Compugen Ltd.
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BU068182
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CA954936
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CL445530
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C1445530 ZMMBBD046
BU067975 1632 E805
BU068295 2556 F04
BU068295 2556 F04
BU068642 2562 H04
BU0686642 2562 E09
CB0039236 As L3 316
AZ141658 SP-0073 B
AZ141658 SP-0073 B
AZ141658 SP-0073 B
AZ1241658 SP-0074 B04
CX989655 BgHC-2.38
CX989655 BgHC-2.38
CX989655 BgHC-2.38
CX989656 As L3 06A
BU067587 1626 F12
CX953980 k1374603.9
BM515619 kj51403.9
BM515619 kj51403.9
        BU066631
CB039563
BM283870
BM568782
CA849289
                                                                                                                                                                                                                              Description
                          1609_B02
1 A8_L3_37H
1 ki28f01.y
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## ALIGNMENTS

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KEYWORDS
SOURCE
ORGANISM
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AG076194
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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                                                                                                                                                                                                   source
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Potoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-911, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1441 bp DNA Pan troglodytes DNA, clone: PTB-070F05.R, AG076194 AG076194.1 GI:16627996 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglodytes
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LIBRARY
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R.Site 2
                                                                                                                                                                                                                                                                      Vector
                                                                                                                                                                                                                                                                                                                                             tracking errors.
                                                                                                                           /organism="Pan troglodytes"
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/db_xref="taxon:9598"
/clone="PTB-070F05.R"
                                                                     /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
                                                                                                                                                                                                                   ce 2 : SacI.
                                                                                                            'sex="male"
   88.9%;
100.0%;
                                                                                                                                                                                                                                                       : pKS145
: SacI
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   Score 16;
Pred. No.
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     DB
14;
                      9;
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                    Length 1441,
                                                                            BAC Library"
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RESULT 3
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                                                                                                                                                          sequence.
BU067975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 Frelinghuysen Road, Piscataway
Tel: 732 445 3801
Fax: 732 445 5736
Email: bharti@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

(bases 1 to 364)

Trail,F., Xu,J.-R., San Miguel,P., Halgren,R.G. and Kistler,H.C. Analysis of expressed sequence tags from Gibberella zeae (anamor Fusarium graminearum)
                                                                                                Gibberella zeae
                                                                                                                               TST
                                                                                                                                                                                     BU067975
1632_E05_J10ZT5 Mature perithecia
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Location/Qualifiers
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The Plant Genome Initiative at Rutgers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Bharti, A.K.
                                                                                                             Gibberella zeae
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                                                                                                                                                                                                                                                                                                                                              83.3%; Score 15; DB llarity 100.0%; Pred. No. 68 Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="ZMMBBb0463D18"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mol_type="genomic DNA"
cultivar="B73"
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Matches 15
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Fungal Genet. Biol. 38 (2), 187-197 (2003)
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Michigan State University
East Lansing, MI 48824, USA
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22508120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
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2556_F04_K08ZT5
                                                                                                                                                                                                                                                                                                     Tel: 517 432 2939
Fax: 517 353 1926
                                                                                                                                                                                                                                                                                                                                East Lansing, MI 48824,
                                                                                                                                                                                                                                                                                                                                   Michigan State University
East Lansing, MI 48824, USA
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Department of Plant Biology
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517 353 1926
                                                                              83.3%; Score 15; DB ilarity 100.0%; Pred. No. 66; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                        trail@msu.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              trail@msu.edu.
                                                                                                                                                                                         /organism="Gibberella:
/mol_type="mRNA"
/strain="NRRL 31084"
/db_xref="taxon:5518"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:5518"
/clone_lib="Mature perithecia"
/note="Vector: ZipLox; Site_1: NotI; Site_2: SalI"
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/strain="NRRL 31084"
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note="Vector: ZipLox; Site_1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trail, F., Xu, J.-R., San Miguel, P., Halgren, R.G. and Kistler, H.C. Analysis of expressed sequence tags from Gibberella zeae (anamorph Fusarium graminearum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 CACGCGACACACTTC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Frances Trail
Department of Plant Biology
Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
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2562_H04_P08ZT5 Mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: trail@msu.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fungal Genet. Biol. 38 (2), 187-197 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gibberella zeae
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                              East Lansing, MI 4
Tel: 517 432 2939
Fax: 517 353 1926
                                                             Contact: Frances Trail
Department of Plant Biology
Michigan State University
East Lansing, MI 48824, USA
                                                                                                                                                             Analysis of expressed sequence tags from G
Fusarium graminearum)
Fungal Genet. Biol. 38 (2), 187-197 (2003)
                                                                                                                                                                                     1 (bases 1 to 414)
1 (bases 1 to 414)
Trail, F., Xu, J.-R., San Miguel, P., Halgren, R.G. and Kistler, H.G.
                                                                                                                                                                                                                                          Eukaryota; Pungi; Ascomycota; Pezizomycotina;
Hypocreomycetidae; Hypocreales; Nectriaceae; C
                                                                                                                                                                                                                                                                              Gibberella zeae
Gibberella zeae
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                                                                                                                                                                                                                                                                                                                                                                            BU068903 414 bp mRNA linear EST 27-A
2569_E09_J17ZTS Mature perithecia Gibberella zeae cDNA, mRNA
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:5518"
/clone_lib="Mature perithecia"
/note="Vector: ZipLox; Site_1: NotI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mol_type="mRNA"
/strain="NRRL 31084"
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 Location/Qualifiers
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RESULT 7
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As L3_31008 SKPL Ascaris suum (parasitic nematode) L3 stage Ascaris suum GDNA cTone As_L3_31G08 5' similar to P41105 60S ribosomal protein L28. Mus musculus (Mouse), mRNA sequence CB039236
                                                                                                                                                                                                                                                                    BACKWARD: T7PL
Plate: 31 row: G
Seq primer: SKPL
High quality sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Blaxter ML
Institute of Cell, Anima
University of Edinburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 440)
Blaxter, M.L., Parkinson, J., Whitton, C., Daub, J., Guilia Blaxter, M.L., Parkinson, J., Whitton, C., Daub, J., Guilia Hall, N., Quayle, M. and Barrell, B.
Edinburgh University/Sanger Centre Nematode EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ascaris suum
                                                                                                                                                                                                                                                                                                                                                                                                           Email: mark.blaxter@ed.ac.uk
The library was prepared for Malcolm Kennedy by Joyce Moore
Glasgow University. Sequencing was performed by the Pathogen
Sequencing Unit, Sanger Centre, Cambridge, UK (Neil Hall, Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3JT, UK.
Tel: +44 131 650 6760
Fax: +44 131 670 5450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea;
Ascaridoidea; Ascarididae; Ascaris
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                                                                                                                                                                                                                                                                        quality sequence stop: 296.
                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:6253"
/clone="As_L3_31G08"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:5518"
/clone_lib="Mature perithecia"
/note="Vector: ZipLox; Site_1: Not1; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Gibberella
/mol_type="mRNA"
/strain="NRRL 31084"
                    /dev stage="L3"
/clone_lib="Ascaris suum (parasitic nematode) L3 stage"
/clone_lib="Ascaris suum (parasitic nematode) L3 stage"
/note="Vector: Lambda ZAP II; Site_1: EcoRI (5'end);
Site_2: (3'end); Ascaris suum is a parasite of pigs. The
library was constructed from mRNA from Ascaris suum L3
stage."
                                                                                                                                                                                                                                                      Location/Qualifiers
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Edinburgh,
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l Hall, Mike
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Query Match Best Local Similarity Matches 15; Conserva

83.3%; Score 15; DB 6; llarity 100.0%; Pred. No. 65; Conservative 0; Mismatches

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REFERENCE
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AZ141658
AZ141658
SP 0003 B1 A08 SP6E Strongylocentrotus purpuratus, purple se urchin, sperm genomic BAC library Strongylocentrotus purpura genomic clone Plate=3 Col=15 Row=B, genomic survey sequence.
AZ141658
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                                           Danio rerio (zebrafish)
Danio rerio
                                                                                      AL924785
AL924785 PJR-Z1+Z2 Danio
AL924785
AL924785.1 GI:23191365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: SP6
Class: BAC ends
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California Institute of Technology
Pasadena California 91125, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ141658.1 GI:8293561 GSS.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: acameron@caltech.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Cameron, RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        additional resources
Proc. Natl. Acad. Sci. U.S.A.
20402566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A sea urchin genome project: Sequence scan,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 449.
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(626) 793-3047
                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                             /clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-
DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Strongylocentrotus
/mol_type="genomic DNA"
/db_xref="taxon:7668"
/clone="Plate=3 Col=15 Row=B"
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100.0%; Pr
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                                                                                                                   452 bp mRNA linear | Danio rerio cDNA clone 145-H10-2,
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Pred. No.
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                                                                                                                                    trail@mgu.edu.
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Contact: Frances Trail
Department of Plant Biology
Michigan State University
East Lansing, MI 48824, USA
Tel: 517 432 2939
Fax: 517 353 1926
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Lab of Functional Genomics
Institute of Molecular and Cell Biology
30 Medical Drive, Singapore, 117609, Singapore
Email: pengjr@imcb.a-star.edu.sg
                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 453)
Trail,F., Xu,J.-R., San Miguel,P., Halgren,R.G. and Kistler,H.C.
Analysis of expressed sequence tags from Gibberella zeae (anamorph
Fusarium graminearum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lo,J., Lee,S., Xu,M., Liu,F., Ruan,H., Eun,A., He,Y., Ma,W., Wang,W., Wen,Z. and Peng,J.
15000 unique zebrafish EST clusters and their future use in microarray for profiling gene expression patterns during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone requests: info@openbiosystems.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Odyssey Drive, Huntsville,
Location/Qualifiers
                                             /organism="Gibberella:
/mol_type="mRNA"
/strain="NRRL 31084"
/db_xref="taxon:5518"
/clone_lib="Mature perithecia"
/note="Vector: ZipLox; Site_1: NotI; Site_2: SalI"
                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="whole embryo or fish"
/dev_stage="mixed stages"
/clone_lib="PJR-Z1+Z2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="local wildtype"
/db_xref="taxon:7955"
/clone="145-H10-2"
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100.0%; Pred. No.
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perithecia
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                                                                                                                                                                                                                                                                                                            184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parasitologie fonctionnelle et evolutive.
CNRS / Univ. Perpignan
52 Ave Paul Alduy, Universite, 66 860 Perpignan cedex, France
Tel: 33 3 68 66 21 88
Fax: 33 3 68 66 22 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata;
Basommatophora; Lymnaeoidea; Planorbidae; Biomphalaria.
1 (bases 1 to 456)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biomphalaria glabrata (bloodfluke planorb)
Biomphalaria glabrata
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BgHC-2.38 BgHC Biomphalaria glabrata
CK989655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitta, G., Galinier, R., Tisseyre, P., Allienne, J.-F., Carmignani, C.
                                                                                                                                                                                   CA954936 459 bp mRNA linear EST 02-JAN-200 kl32e04.yl Ascaris suum embryo SL1 TOPO vl Ascaris suum cDNA 5' similar to SW:RL28_MOUSE P41105 60S RIBOSOMAL PROTEIN L28. ;, mRNA
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1 (bases 1 to 459)
McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
                                                                                 Ascaris suum (pig roundworm)
Ascaris suum
                                                                                                                                                     cA954936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mitta@univ-perp.fr
Seq primer: CGAAGTTATCTCGACG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mitta Guillaume
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2004
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                                                 Ascaridoidea; Ascarididae; Ascaris.
                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;
                                                                                                                                     CA954936.1 GI:27471296
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Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pDNR-LIB; The library was designed with ng of total RNA using the creator SMART cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                construction kit (Clontech)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Circulating hemocytes"
/clone_lib="BgHC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Biomphalaria glabrata"
|mol_type="mRNA"
/isoTate="Bg.Bra strain"
/db_xref="taxon:6526"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="hermaphrodite"
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The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: estawatson.wustl.edu

Email: estawatson.wustl.edu

The library was constructed by Claire Murphy and Dr. James McCarter

at Washington University, St. Louis. Oligo(dT)-SL1 PCR based

at Washington University, St. Louis. Oligo(dT) on ucleotides

containing SL1 on the 5' end and oligo(dT) on the 3' end were

containing SL1 on the 5' end and oligo(dT) on the 3' end were

non-directionally cloned into pCRII-TOPO(Invitrogen) following the

Topo TA cloning protocol. 30-60 cell embryo material was provided

by Dr. Richard Davis of City University of New York Graduate

by Dr. Richard Davis of Staten Island, Staten Island, NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 CACGCGACACACTTC 18
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Fax: 314 286 1810
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                   As_L3_06A09 SKPL Ascaris suum (parasitic nematode) L3 stage suum cDNA clone As L3_06A09 5' similar to ref[NP_033107.1] ribosomal protein L28 - Mus musculus, mRNA sequence.
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Blaxter, M.L., Parkinson, J., Whitton, C., Daub, J., Guiliano, D., Hall, N., Quayle, M. and Barrell, B. Edinburgh University/Sanger Centre Nematode EST Project Unpublished (2000)
                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;
                                                                                                                                                                                                                            Ascaris suum (pig roundworm)
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                                                                                                                                            Ascaridoidea; Ascarididae; Ascaris.
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                                                                                                                 (bases 1 to 477)
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/clone lib="Ascaris suum embryo SL1 TOPO v1"
/note="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI;
/note="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI;
/note 2: EcoRI; The library was constructed by Claire
Murphy and Dr. James McCarter at Washington University,
St. Louis. Oligo(dT)-SL1 PCR based library. Embryo cDNA
PCR products of size >400 nucleotides containing SL1 on
the 5' end and oligo(dT) on the 3' end were
non-directionally cloned into pCRII-TOPO(Invitrogen)
following the Topo TA cloning protocol. 30-60 cell embryo
material was provided by Dr. Richard Davis of City
University of New York Graduate Center, College of Staten
Island, Staten Island, NY (redavis@postbox.csi.cuny.edu)."
                                                                                                                                                                                                       anna
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/lab_host="DH10B"
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/db_xref="taxon:6253"
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100.0%; Pred. No.
Live 0; Mismatc
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EST 02-JAN-2003

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BU067587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road,
                                                                                                                                                                                                                                                                                                                                       Trail,F., Xu,J.-R., San Miguel,P., Halgren,R.G. and Kistler,H.C. Analysis of expressed sequence tags from Gibberella zeae (anamorph Fusarium graminearum)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gibberella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BU067587 481 bp mRNA linear EST 1626_F12_K24ZT5 Mature perithecia Gibberella zeae cDNA,
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Plate: 06 row: A
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                                                                                                                                                                                                        Michigan State University
                                                                                                                                                                                                                             Department of Plant Biology
                                                                                                                                                                                                                                                     Contact: Frances Trail
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                                                                                                                                   t Lansing, MI 4: 517 432 2939
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+44 131 670 5450
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                                                                                                              trail@msu.edu.
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/clone_lib="Ascaris suum (parasitic nematode) L3 stage"
/note="Vector: Lambda ZAP II; Site_1: EcoRI (5'end);
Site_2: (3'end); Ascaris suum is a parasite of pigs. The
library was constructed from mRNA from Ascaris suum L3
stage."
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/mol_type="mRNA"
/db_xref="taxon:6253"
/organism="Gibberella zeae"
/mol_type="mRNA"
/strain="NRRL 31084"
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100.0%; Pr
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McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,

Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,

Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,

Tasgareishvili,R., Ronko,I., Kennedy,S., Magnire,L., Beck,C.,

Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,

Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,

McCann,R., Waterston,R. and Wilson,R.

The Washington Univ. Nematode EST Project, 1999

Unpublished (1999)
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CA953980

A83 bp mRNA linear EST 02-JAN-200 kl37a10.yl Ascaris suum embryo SL1 TOPO vl Ascaris suum cDNA 5' similar to SW:RL28 MOUSE P41105 60S RIBOSOMAL PROTEIN L28. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 CACGCGACACACTTC 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarte
at Washington University, St. Louis. Oligo(dT)-SL1 PCR based
library. Embryo cDNA PCR products of size >400 nucleotides
containing SL1 on the 5' end and oligo(dT) on the 3' end were
non-directionally cloned into pCRII-DOPO(Invitrogen) following the
Topo TA cloning protocol. 30-60 cell embryo material was provided
by Dr. Richard Davis of City University of New York Graduate
Center, College of Staten Island, Staten Island, NY
(redavis@postbox.csi.cuny.edu).
                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: SL1 primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: McCarter JP
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  /clone lib="Ascaris suum embryo SL1 TOPO v1"
/note="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI;
Site 2: EcoRI; The library was constructed by Claire
Murphy and Dr. James McCarter at Washington University,
St. Louis. Oligo(dT)-SL1 PCR based library. Embryo cDNA
PCR products of size >400 nucleotides containing SL1 on
the 5' end and oligo(dT) on the 3' end were
non-directionally cloned into pCRII-TOPO(Invitrogen)
following the Topo TA cloning protocol. 30-60 cell embryo
material was provided by Dr. Richard Davis of City
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/clone_lib="Mature perithecia"
/note="Vector: ZipLox; Site_1: Not1; Site_2:
                                                                                                                                                                                                                                  /mol_type="mRNA"
/db xref="taxon:6253"
/db ystage="30-60 cell embryo"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                         organism="Ascaris suum"
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James McCarter

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University of New York Graduate Center, College of Staten Island, NY (redavis@postbox.csi.cuny.edu)."
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ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CACGGGAACTTC 18

Search completed: February 10, 2005, 17:01:56 Job time : 124.68 secs

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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna//US06_NEW_PUB.seq:*
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/ Cgn2 6/ptodata/1/pubpna/US10E PUBCOMB.seq: *
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Sequence 1, Appri Sequence 1183, Ap	Sequence 14852, Aps	Sequence 114310, Sequence 33178, A	Sequence 10, Appl Sequence 8, Appli Sequence 8, Appli	Description

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Sequence 14408, A Sequence 15589, A Sequence 1844, Ap Sequence 25898, A Sequence 4958, Ap Sequence 4958, Ap Sequence 57089, A		. 60 60 60 - 6		Sequence 31761, A Sequence 40730, A Sequence 1395, Ap Sequence 10564, A Sequence 1540, Ap Sequence 279, App Sequence 30016, A Sequence 30016, A

# ALIGNMENTS

US-09-872-051-10

GENERAL INFORMATION:

Sequence 10, Application US/09872051 Patent No. US20020013960A1

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APPLICANT: Monsanto Co
APPLICANT: Behr, Carl
APPLICANT: Heronaka, Catherine
APPLICANT: Hronaka, Catherine
APPLICANT: You, Jinsong
APPLICANT: You, Jinsong
TITLE OF INVENTION: Thereof
FILE REFERENCE: 38-21(5258)B
CURRENT APPLICATION NUMBER: US/09/872,051
CURRENT APPLICATION NUMBER: US/09/872,051
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/240,014
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/240,014
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Best Local
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Patent No. US20020013960A1
GENERAL INFORMATION:
                                                   TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and TITLE OF INVENTION: Thereof FILE REFERENCE: 38-21(52258)B CURRENT APPLICATION NUMBER: US/09/872,051 CURRENT FILING DATE: 2001-06-01 PRIOR APPLICATION NUMBER: 60/213,567 PRIOR EPILICATION NUMBER: 60/213,567 PRIOR FILING DATE: 2000-06-22
                                                                                                                                                                                                                                                                                                                                          09-872-051-8
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PRIOR TILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR PILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/240,014
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APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods
TITLE OF INVENTION: Thereof
TITLE OF INVENTION INTEREOF
FILE REFERENCE: 38-21(52258)8
CURRENT APPLICATION NUMBER: US/10/790,430
CURRENT FILING DATE: 2004-03-01
               PRIOR APPLICATION NUMBER: 60/241,215 PRIOR FILING DATE: 2000-10-13
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APPLICANT: Behr, Carl
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APPLICANT: Behr, Carl
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NAME/KEY: Source
NOCATION: (1)..(18)
OTHER INFORMATION: zea maize plastid DNA and vector
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APPLICATION NUMBER: 60/240,014
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You, Jinsong
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Hironaka, Catherine
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FEATURE:

NAME/KEY: Source

NAME/KEY: Source

LOCATION: (1)..(1183)

OTHER INFORMATION: 1-164 Agrobacterium tumefaciens n
OTHER INFORMATION: 165-381 construct vector DNA
OTHER INFORMATION: 382-686 Zea maize plastid genes,
OTHER INFORMATION: 687-1183 Zea maize genomic DNA
US-09-872-051-8
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Best Local S
Matches 18
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Best Local Similarity
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SOFTWARE: PatentIn version
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PRIOR APPLICATION NUMBER: 60/213,567
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR APPLICATION NUMBER: 60/240,014
PRIOR APPLICATION NUMBER: 60/240,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Heck, Gregory
APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods
TITLE OF INVENTION: Thereof
FILE REFERENCE: 38-21(52258) B
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                   NAME/KEY: source
LOCATION: (1)..(1183)
LOCATION: (1)..(1183)
OTHER INFORMATION: 1-164 Agrobacterium tumefaciens nos 3'
OTHER INFORMATION: 165-381 construct vector DNA
OTHER INFORMATION: 382-686 Zea maize plastid genes, rps11
OTHER INFORMATION: 687-1183 Zea maize genomic DNA
                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
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RESULT 5 US-10-425-115-114310

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US-10-369-493-33178/c
; Sequence 33178, Application US/10369493
; Publication No. US20030233675A1
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; OTHER INFORMATION: Clone ID: MRT4577_35734C.1
US-10-425-115-114310
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                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Xylella fastidiosa
US-10-369-493-33178
                                                                                                                                                                US-10-653-047-1012
                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10 (52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NO 33178
SEQ ID NO 33178
LENGTH: 1338
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LENGTH: 466
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                                                                                                   Sequence 1012, Application US/10653047 Publication No. US20040229367A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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APPLICANT: Hinl
APPLICANT: Sla
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                                                            APPLICANT: Randy M. Berka APPLICANT: Michael W. Rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Zea mays
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                                                                                                                                                                                                                                                  513 ACCACGCGACACACTT 498
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Slater, Steven C.
Soldman, Barry S.
Chen, Xianfeng
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Michael W. Rey
Jeffrey R.Shuster
Sakari Kauppinen
Ib Groth Clausen
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Sequence 753, Application No. US200 GENERAL INFORMATION:

Application US/10781014 o. US20040180408A1

APPLICANT: Pompejus, Markus APPLICANT: Kroger, Burkhard APPLICANT: Schroder, Hartwis APPLICANT: Zelder, Oskar

Schroder, Hartwig Zelder, Oskar

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CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 14852
LENGTH: 721
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(721)
OTHER INFORMATION: unsure at all n locations
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1012
LENGTH: 687
TYPE: DNA
ORGANISM: Pusarium venenatum
US-10-653-047-1012
RESULT 9
US-10-781-014-753/c
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US-10-425-115-14852
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Best Local S
Matches 15
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Publication No. US20040214272A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2003-08-29
FRIOR APPLICATION NUMBER: US/09/533,559
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/273,623
PRIOR FILING DATE: 1999-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 5849.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_113531C.1
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mes 15; Conserv
                                                                                                                                                                Local Similarity
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                                                                             476 CACGCGACACACTTC 490
                                                                                                                                                   15;
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100.0%; Pr
                                                                                                                                                                  83.3%;
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                                                                                                                                                                      Score 15; DB 1; Pred. No. 6.3;
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                                                                                                                                                                                       DB 18;
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OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS

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          APPLICANT: KEDĀ, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
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Best Local Similarity
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LENGTH: 747
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NUMBER
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PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
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CURRENT FILING DATE: 2004-02-17
                                                                                                                                                                                                                                                                               APPLICANT:
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NAME/KEY: CDS
LOCATION: (101)..(724)
OTHER INFORMATION: RXN02554
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APPLICATION NUMBER: DE 19931420.9
FILING DATE: 1999-07-08
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APPLICATION NUMBER: DE 19931428.4
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APPLICATION NUMBER: DE 19931412.8
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SEQ ID NOS: 7059
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TATEISHI, NAOKO
SENOH, AKIHIRO
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OCHIAI, KEIKO
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100.0%; Pr/
0;
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Pred. No.
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; Sequence 31761, Application US/10357930
; Publication No. US20040259086A1
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TITLE OF INVENTION: No. US20040009474Alel Human Polynucleotides and Polypeptides

FILE REFERENCE: 21402-012

CURRENT APPLICATION NUMBER: US/09/864,408A

CURRENT FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: 60/206,690

PRIOR APPLICATION NUMBER: 60/206,690

PRIOR FILING DATE: 2000-05-24

NUMBER OF SEQ ID NOS: 9068

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1183
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Matches :
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                                                                                                                                                                                                                                                   APPLICANT: MODAĥAN, JOĤN
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS,
TITLE OF INVENTION: IDENTIFICATION, ASSESSMEN
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007DCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schlegel. Robert APPLICANT: Endege, Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Leach, Martin D. APPLICANT: Shimkets, Richa
                                    PRIOR
                                                                                            PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Corynebacterium glutamicum
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PRIOR FILING DATE: 2000-02-17
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                         APPLICATION NUMBER: 60/211,314
                                  APPLICATION NUMBER: 60/219,007
                                                         FILING DATE:
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NUMBER: 60/255,281
                                                         2000-06-09
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100.0%; Pred. No.
Live 0; Mismatcl
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T, PREVENTION,
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; ORGANISM: Homo sapiens
US-10-357-930-31761
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                                                                                                                                                                RESULT 14
US-10-357-930-1395/c
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CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
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NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 31761
                                 Sequence 1395, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40730
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: LIBENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
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  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
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, John
NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
IDENTIFICATION, ASSESSMENT, PREVENTION, AND
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100.0%; Pred. No.
tive 0; Mismatci
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CURRENT FILING DATE: 2003-02-04
CURRENT FILING DATE: 2003-02-04
CURRENT FILING DATE: 2003-02-06
PRIOR APPLICATION NUMBER: 09/785, 276
PRIOR FILING DATE: 2003-02-16
PRIOR PELICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
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                                                                                                                                     PRIOR APPLICATION NUMBER: 09/785,276
PRIOR PILLING DATE: 2003-02-16
PRIOR PILLING DATE: 2003-02-16
PRIOR PILLING DATE: 2000-02-17
PRIOR PILLING DATE: 2000-02-17
PRIOR PILLING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR PILLING DATE: 2000-05-25
PRIOR PILLING DATE: 2000-05-25
PRIOR PILLING DATE: 2000-06-09
PRIOR PILLING DATE: 2000-06-09
PRIOR PILLING DATE: 2000-06-09
PRIOR PILLING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/255,281
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 36, 86, 87
OTHER INFORMATION: n = A,T,C o
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                                                    NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10564
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APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILLING DATE: 2003-02-04
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PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version
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LENGTH: 484
TYPE: DNA
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US-10-357-930-10564

Query Match
Best Local Similarity 100.0%; Pred. No. 28;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CACGCGACACACTT 17
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Db 335 CACGCGACACACTT 322

Search completed: February 9, 2005, 11:12:45
Job time: 34.935 secs

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Minimum DB :
Maximum DB :
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Perfect score:
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Gapop_60.0 , Gapext 60.0
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19
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Copyright (c) 1993 - 2005 Compugen Ltd.
                  n2 6/ptodata/1/pubpna/US09A PUBCOMB.seq:*
gn2 6/ptodata/1/pubpna/US09B PUBCOMB.seq:*
gn2 6/ptodata/1/pubpna/US09B PUBCOMB.seq:*
gn2 6/ptodata/1/pubpna/US090 PUBCOMB.seq:*
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gn2 6/ptodata/1/pubpna/US10B PUBCOMB.seq:*
gn2 6/ptodata/1/pubpna/US10C PUBCOMB.seq:*
gn2 6/ptodata/1/pubpna/US10C PUBCOMB.seq:*
gn2 6/ptodata/1/pubpna/US10E PUBCOMB.seq:*
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gn2 6/ptodata/1/pubpna/US10E PUBCOMB.seq:*
gn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*
gn2 6/ptodata/1/pubpna/US11 NEW PUB.seq:*
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6/ptodata/1/pubpna/US06 PUBCOMB.seq:*
6/ptodata/1/pubpna/US07 NEW PUB.seq:*
6/ptodata/1/pubpna/PCTUS PUBCOMB.seq:*
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6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Result No.
15 15 16 16 16 16 16 16 16 16 16 16 16 16 16	Score
100.0 100.0 100.0 100.0 84.2 84.2 84.2 84.2 78.9 78.9	Query Match
19 498 498 1044 35167 35167 902560 521 1339	Query Match Length DB ID
9 18 18 15 18 18 18 18	80
9 US-09-872-051-9 18 US-10-790-430-9 9 US-09-872-051-7 18 US-10-790-430-7 15 US-10-156-761-1684 18 US-10-645-794-5 18 US-10-645-983A-1 17 US-10-156-761-3339 18 US-10-424-599-43339 18 US-10-424-599-43339 18 US-10-437-963-26588	ID
Sequence 9, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1684, Ap Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 43, Ap Sequence 26388, A	Description

Query Match

100.0%; Score 19;

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US-10-925-095-556	-10-472-362-2	US-09-826-509-556	-10-282-122A-	-10-424-599-12714	-10-260	-10-425	824	-963-	US-10-437-963-90735	US-10-437-963-9105	US-10-425-115-164400		US-10-425-115-55360	US-10-767-795-5965	US-10-767-701-23177	10-437-963-	US-10-424-599-127151	US-09-754-997A-43	US-10-425-115-29397	US-10-029-386-25290	US-09-983-965-2307	US-09-918-995-17011	US-10-425-115-174641	US-10-424-599-79875	US-09-960-352-7737	US-10-369-493-32240	US-09-983-965-4908	US-10-425-115-47913	US-10-425-115-172757	US-10-473-390-3	US-10-437-963-60106	-10-473-390-1	
Sequence 556, App	e 2, Ap	000	0 F40/4	e 12/149,	0	176765		85113	90735,	9105, 7	164400	61015	55360,		23177,	25717,		4	29	Sequence 25290, A		Sequence 17011, A	Sequence 174641,	Sequence 79875, A	7737, Ap	Sequence 32240, A	4908, Ap	4791	е Ц		6	, ,_	

# ALIGNMENTS

US-09-872-051-9

GENERAL INFORMATION:
APPLICANT: Monsanto Co

Sequence 9, Application US/09872051 Patent No. US20020013960A1

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APPLICANT: Behr, Carl
APPLICANT: Hiromaka, Catherine
APPLICANT: Heck, Gregory
APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Det
TITLE OF INVENTION: Thereof
FILE REFERENCE: 38-21(52258)B
CURRENT APPLICATION NUMBER: US/09/872,051
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
LENGTH: 19
TORANISM: Artificial Sequence
FEATURE:
NAME/KEY: source
IOCANION: (1) . . (19)
OTHER INFORMATION: Zea maize genomic and vector DNA
US-09-872-051-9
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Best Local Similarity

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US-09-872-051-7
; Sequence 7, Application US,
; Patent No. US20020013960A1
; GENERAL INFORMATION:
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APPLICANT: You, Jinsong

TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Com

TITLE OF INVENTION: Thereof

FILE REFERENCE: 38-21(52258)B

CURRENT APPLICATION NUMBER: US/10/790,430

CURRENT APPLICATION NUMBER: US/09/872,051

PRIOR APPLICATION NUMBER: US/09/872,051

PRIOR APPLICATION NUMBER: 60/213,567

PRIOR FILING DATE: 2000-06-22

PRIOR APPLICATION NUMBER: 60/241,215

PRIOR APPLICATION NUMBER: 60/241,215

PRIOR APPLICATION NUMBER: 60/241,215

PRIOR FILING DATE: 2000-10-13

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Matches
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                                                         FILE REFERENCE: 38-21(52258)B
CURRENT APPLICATION NUMBER: US/09/872,051
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/241,215
                                                                                                                                                                                      APPLICANT: Hironaka, Catherine
APPLICANT: Heck, Gregory
APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Detec
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/240,014
PRIOR FILING DATE: 2000-10-13
                                                                                                                                                                                                                                                                                                APPLICANT: Monsanto Co
APPLICANT: Behr, Carl
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NUMBER OF SEQ ID NOS: 16
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APPLICANT: Behr, Carl
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OTHER INFORMATION: Zea maize genomic and vector DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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19; Conserv
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100.0%; Pred. No. 0.041;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 7
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                                                                           Matches
                                                                                                                  Query Match
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APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Detec
TITLE OF INVENTION: Thereof
FILE REFERENCE: 38-21(52258)B
CURRENT APPLICATION NUMBER: US/10/790,430
CURRENT FILING DATE: 2004-03-01
PRIOR APPLICATION NUMBER: US/99/872,051
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2000-06-02
PRIOR PILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR APPLICATION NUMBER: 60/240,014
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APPLICANT: Behr, Carl
APPLICANT: Hironaka, C
APPLICANT: Heck, Grego
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                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0
                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: source
LOCATION: (1)..(498)
OTHER INFORMATION: 1-304 Zea maize genomic DNA
OTHER INFORMATION: 305-349 construct vector DNA
OTHER INFORMATION: 350-498 rice actin 1 promoter
                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 16
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FEATURE:
NAME/KEY: SOURCE
LOCATION: (1). (498)
OTHER INFORMATION: 1-304 Zea maize genomic DNA
OTHER INFORMATION: 305-349 construct vector DNA
OTHER INFORMATION: 350-498 rice actin 1 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                                                                           1 Similarity
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TGTAGCGGCCCACGCGTGG
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                                                                             Conservative
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                                                                                              100.0%; Score 19; 100.0%; Pred. No.
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100.0%; Pred. No.
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                                                                             Mismatches
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                                                                                              0.021;
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RESULT 5 US-10-156-761-1684/c ; Sequence 1684, Application US/10156761 ; Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO

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                                                                                             US-10-645-794-5
                                                                                                                                                                                                                                                                                       FILE REFERENCE: 20699Y
CURRENT APPLICATION NUMBER: US/10/645,794
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: 60/458,825
PRIOR FILING DATE: 2003-03-28
PRIOR FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: 60/455,312
PRIOR FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: 60/455,234
PRIOR FILING DATE: 2003-03-17
PRIOR FILING DATE: 2003-03-17
PRIOR FILING DATE: 2003-03-17
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Best Local Similarity
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LENGTH: 1044
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 16; Conservative
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Query Match 84.2%; Score 16; DB 18; Length 35167; Best Local Similarity 100.0%; Pred. No. 0.67; Matches 16; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                  SOFTWARE: F
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS FOR PROPAGATING ADENOVIRUS AND TITLE OF INVENTION: VIRUS PRODUCED THEREBY FILE REFERENCE: 20699Y
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                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/405,182 PRIOR FILING DATE: 2002-08-22
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NAME/KEY: CDS
LOCATION: (1)..(1044)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                             TYPE: DNA ORGANISM: adenovirus serotype 24
                                                                                                                                                         LENGTH: 35167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 TAGCGGCCCACGCGTG 344
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                                                                                                                                                                                                       FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaslow, David C.
Morsy, Manal
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Sandig, Volker
Emini, Emilio A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Casimiro, Danilo R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shiver, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.2%; Score 16; DB 15; Length 1044; 100.0%; Pred. No. 1.4;
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APPLICANT: HORKKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FULRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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Publication No. US20030119018A1
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Best Local Similarity
                                                                                                                                                                                              SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/645,883A
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: 60/455,312
PRIOR FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 15
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ADENOVIRUS SEROTYPE 24 VECTORS, NUCLEIC TITLE OF INVENTION: ACIDS AND VIRUS PRODUCED THEREBY FILE REFERENCE: 21366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Emini, Emilio A.
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                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: (4187715)
OTHER INFORMATION: a, t
                                                                                                                                                        TYPE: DNA
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                                                                                                                                  ORGANISM: Streptomyces avermitilis
                                                                                                                                                                            LENGTH: 9025608
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Morsy, Manal
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No. US20040185555A1
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    84.2%;
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      Score 16;
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      DB 15;
      Length 9025608;
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RESULT 11
US-10-437-963-26588/c
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_139133C.1
US-10-424-599-43339
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US-10-767-701-9887
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 43339
LENGTH: 521
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (53535)5
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
                                                                                                                                                Matches
                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                         SEQ ID NO 9887
LENGTH: 797
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Best Local (
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                                                                                                                                                                                                                                                                       ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                        195 GTAGCGGCCCACGCG 181
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15; Conserv
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                                                                                                                                                Conservative
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Pred. No.
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; Mismatches
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US-10-437-963-33098
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                                                                                                                                                                                                                                              SEQ ID NO 33098
LENGTH: 1398
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SEQ ID NO 26588
                                                                                            Query Match
Best Local (
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Best Local (
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                                                                            Matches
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                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT FILION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966
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APPLICANT:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: wu, Wei
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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ORGANISM: Oryza sativa
                                                                                                                                                                                        TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
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                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 78.9%; Score 15; DB 18; Length 1339;
l Similarity 100.0%; Pred. No. 5.4;
15; Conservative 0; Mismatches 0; Indels
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                                    4 AGCGGCCCACGCGTG 18
                                                                                              Similarity
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Barbazuk, Brad
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                                                                          Conservative
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                                                                                              78.9%; Score 15; DB 18; Length 1398; 100.0%; Pred. No. 5.3;
603
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                                                                              Mismatches
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RESULT 13 US-10-473-390-1/c ; Sequence 1, Application US/10473390

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; Sequence 60106, Application US/10437963
; Publication No. US20040123343A1
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                                                                                                      RESULT 15
US-10-473-390-3/c
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                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61666C.1
US-10-437-963-60106
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
APPLICANT: Note and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221) B
CURRENT APPLICATION UNMERR: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 60106
LENGTH: 5013
TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
SEQ ID NO 1
Sequence 3, Application US/10473390
Publication No. US20040248112A1
GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen M. et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Matches 15; Conservative (
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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001206-US
CURRENT APPLICATION NUMBER: US/10/473,390
CURRENT FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: PCT/US02/09743
PRIOR PILING DATE: 2002-04-01
PRIOR FILING DATE: 2002-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/820,923
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ORGANISM: Homo sapiens
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Local Similarity 100.0%; Pred. No. 4.1;
hes 15; Conservative 0; Mismatches 0; Indels
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Cao, Yongwei
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Search completed: February
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LENGTH: 14800
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                    Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: CL001206-US
CURRENT APPLICATION NUMBER: US/10/473,390
CURRENT FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: PCT/US02/09743
PRIOR FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 09/820,923
PRIOR FILING DATE: 2001-03-30
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                     2050 AGCGGCCCACGCGTG 2036
                                                                                                      4 AGCGGCCCACGCGTG 18
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                                                                                                                                      78.9%; Score 15;
100.0%; Pred. No.
tive 0; Mismatcl
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Perfect score:
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Copyright (c) 1993 - 2005 Compugen Ltd.
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geneseqn2003ds:*
geneseqn2004as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

The invention relates to a DNA construct (I) a second (F2) expression cassette. F1 of the

comprising a first (F1) and DNA construct, in operable

Claim 8; Page 3; 25pp; English.

Novel DNA construct useful for producing a corn plant that tolerates application of glyphosate herbicide, comprises two transgene expression

WPI; 2002-165871/22.

Behr CF,

Hironaka C,

Heck GR,

You Ġ,

c 45		43	42		c 40	39		c 37			34	33	32		c 30		28	c 27			c 24	23	22	21
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ADA68658	ABL02754	ACF64545	AAS59616	ABL19130	ABL32202	ABL15162	ABL04600	ABL15163	ABL04601	ABZ17153	ACA26538	AAS88878	ABQ54083	ABQ54082	ADL12097	ADG73042	ABQ35645	ABQ35644	ABQ35495	ABQ35494	ABQ45114	ABQ45115	ADS54342	ABQ98333
Ada68658 Takirugu													Abq54083 Oligonuci	Abq54082 Oligonuci	AGIIZO9/ PSeudomon				-		_		N	Abq98333 Human ORF

# ALIGNMENTS

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RESULT 1
ABK15247
Probe; ss; rice actin 1 promoter; RA1; RA1 intron; chloroplast transit peptide gene; glyphosate resistance; corn; 5-enol-pyruvylshikimate-3-phosphate synthase; EPSPS; Hsp70 intron; transcriptional terminator; cauliflower mosaic virus 35S promoter; pv-ZMGT32; transgenic; nk603.
                                                                                                                                                                                                                                         Zea mays.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                    ABK15247;
                                                                                                                                           22-JUN-2000; 2000US-0213567P.
13-OCT-2000; 2000US-0240014P.
13-OCT-2000; 2000US-0241215P.
                                                                                                                                                                                15-JUN-2001; 2001EP-00202314.
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                                                                                                                          (MONS ) MONSANTO TECHNOLOGY LLC.
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RESULT 2
ABK15245
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Best Local
                                                   22-JUN-2000;
13-OCT-2000;
13-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     5-enol-pyruvylshikimate-3-phosphate synttenscriptional terminator; cauliflower pv-ZMGT32; transgenic; nk603.
Behr CF,
                                                                                                                                                                                                                                                                                           misc_feature
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Escherichia
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                          (MONS ) MONSANTO
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Hironaka
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2000US-0240014P.
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687. .1183
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                          TECHNOLOGY LLC
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382. .686
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Heck GR,
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Mismatches
You J;
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te synthase; EPSPS; Hsp70 int
flower mosaic virus 35S promo
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ADS57504/c
ID ADS57504 standard; cDNA; 1338 BP.
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WPI;
                                                 Cao
                                                                                                 (HINK/)
(SLAT/)
(CHEN/)
(GOLD/)
                                                                                                                                                                                                                                                       21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                                                                                                                                                                            US2003233675-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant DNA construct; transformed plant; improved plant cold tolerance; heat tolerance; drought tolerance; herbicide; pathogen tolerance; pest tolerance; plant disease resistance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria
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2004-061375/06
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GOLDMAN B S
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PB;

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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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Claim 1; SEQ ID NO 33178; 122pp; English.

CC microbial source: The invention also relates to a transformed plant CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC having an improved property comprises transforming a plant with the CC recombinant DNA construct and growing the transformed plant, where the CC polynucleotide or polypeptide is useful for improving plant with the CC improved plant properties, e.g. improved cold, heat or drought tolerance, CC interance to herbicides, extreme osmotic conditions, pathogens or pests, CC increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of CC content, improved yield by modification of carbohydrate, nitrogen or CC condition, improved plant growth and development under at least one stress CC condition, improved lignin production or improved galactomannan CC production. This sequence represents a bacterial polymucleotide used in CC condition, improved lignin production or improved galactomannan CC production. This sequence represents a bacterial polymucleotide used in CC format from USPTO at seqdata.uspto.gov/sequence.html. promoter functional in a plant cell, where the promoter is positioned provide for expression of a polynucleotide encoding a polypeptide from The invention relates to a recombinant DNA construct comprising a to

Sequence 1338 BP; 241 A; 281 C; 463 G; 353 T; 0 U; 0 Other;

Query Match Best Local S Matches 16 l Similarity 88.9%; Score 16; ilarity 100.0%; Pred. No. Conservative 0; Mismatc Mismatches 2.9; DB 13; Length 1338; 0; Indels 0 0

밁 Ś 513 N ACCACGCGACACACTT 17 ACCACGCGACACACTT 498

AAF08489 standard; cDNA; 687

AAF08489;

13-MAR-2001 (first entry)

EST SEQ ID NO:1012.

Fusarium venenatum

RESULT 4
AAFORAMP
IID AAAP
XX AAFOR
XX AAFOR
XX FUSS
DT 13-H
XX FUSS
XX Mult
KW Mult
KW Cull
KW ASpp
KW Cull
XX W
CUL
XX BUSS
SUSS
EUSS
XX WO21
XX BUSS
XX WO21
XX WO2 Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.

Fusarium venenatum.

WO200056762-A2

22-MAR-2000; 2000WO-US007781.

22-MAR-1999; 9908-00273623

(NOVO ) NOVO NORDISK BIOTECH INC (NOVO ) NOVO NORDISK AS.

WPI; 2000-594572/56.

Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags.

Claim 86; Page 768; 3161pp; English

The present invention describes a method for monitoring differential CC expression of genes in a first filamentous fungal (FF) cell relative to cells. The method uses fluorescence-labeled nucleic acids isolated from CC cells. The method uses fluorescence-labeled nucleic acids isolated from CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs care used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of genes CC same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential cof the microorganisms to be improved. New genes may be discovered, conditions, environmental stress, spore morphogenesis, recombination, cometabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of canditions, as one spot on an array equals one gene or open reading frame, can be compared to facilitate analysis of the results. AAF07478 to AAF11247 con Aspergillus oryzae; and AAF14879 to AAF12487 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF1337 represents ESTs from control of the present of

Sequence 687 BP; 167 A; 190 C; 152 G; 178 T; 0 U; 0 Other;

Matches Query Match 15; Similarity Conservative 83.3%; 0 Score 15; Pred. No. Mismatches DB ω --0; Length 687 Indels 0 Gaps 0

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531 CACGCGACACACTTC 545

4

CACGCGACACACTTC 18

AAF71736 standard; DNA; 747

AAF71736;

30-APR-2001 (first entry)

Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:753

RESULT 5
AAF71736/c
ID AAF717
XX
AAF7177
AC AAF717
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DT 30-APR
COryne
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COryne
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COryne
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SMP px
KW fine c
KW fine c
KW nuclee
KW carboh
KW carboh
KW diagna
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COryne
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OS O1-JAN
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XX
O1-JAN
XX
O8-JUL
PR 23-JUL
PR 25-JUL
PR 08-JUL diagnosis; Corynebacterium diphtheriae; evolutionary nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid;

Corynebacterium glutamicum.

23-JUN-2000; 2000WO-IB000943

25-JUN-1999; 08-JUL-1999; 99US-0141031P 99DE-01031412

B-JUL-1999; B-JUL-1999; B-JUL-1999; B-JUL-1999;

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                                                                                                    AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar CC metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 cc to AAB 79633 which are involved in carbon metabolism and energy cc production. The C glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or comproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a cc a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a cc polyketide, or an enzyme. The presence of (I) or SMP proteins (III) c encoded by them are used for diagnosing the presence or activity of c containing them are used for map genomes of organisms related to C. containing them are used to map genomes of organisms related to C. glutamicum, identify and localise C. glutamicum sequences of interest, in cevolutionary studies, in determining SMP protein regions required for metabolism of sugars, and in modulating high-energy molecule production in a cell (i a ATP) ANDRH).
                                               Query Match
Best Local S
Matches 15
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03-SEP-1999;
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03-SEP-1999;
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14-JUL-1999;
27-AUG-1999;
31-AUG-1999;
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3-JUL-1999;
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DB; AAB79619.
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              CACGCGACACACTTC
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99US-0143208P

99DE-01032974

99DE-01032973

99DE-01033005

99DE-01040775

99DE-01042076

99DE-01042086

99DE-01042086

99DE-01042088

99DE-01042088

99DE-01042123

99DE-01042123
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or
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C glutamicum

coding

sequence fragment SEQ ID NO: 7068

bacterium;

amino

acid synthesis; vitamin; saccharide;

26-SEP-2001

(first

entry)

0

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ARESULT 7
AAH68533/c
ID AAH685
XX
AAH685
XZ
AC AAH685
XZ
DT 26-SEP
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                               The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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Tateishi
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                                                                                                                                                                                                                                                          Sequence
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Senoh A, Ikeda
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2000JP-00280988
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Tateishi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum
                                                                                                                 canine microarray; drug screening; toxicity assay; environmental pollutant; cellular response; gene expression profile; toxic response; liver necrosis; fatty liver disease; protein adduct formation; hepatitis; dog; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 349980 BP; 81250 A; 97718 C; 90621 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-376931/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2000; 2000EP-00127688
                                                                                     Canis familiaris
                                                                                                                                                                                                                        21-OCT-2004
05-MAY-2003; 2003WO-US013853.
                                                        WO2004063324-A2
                                                                                                                                                                                          Novel canine microarray-related DNA sequence SeqID6234.
                                                                                                                                                                                                                                                                                                                                                          328188
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention provides a number of nucleotide and protein com the Coryneform bacterium Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 7068; 246pp + Sequence Listing; English
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2000JP-00159162.
2000JP-00280988.
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Senoh A, Ikeda
                                                                                                                                                                                                                        (first entry)
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da M,
                                                                                                                                                                                                                                                                                   ВP
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Pred. No.
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Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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RESULT 9 ABV40711/c

ABV40711 standard; cDNA;

435

**B**P

16-SEP-2002 ABV40711;

(first entry

Human prostate expression marker cDNA 40702

Human; prostate pharmacogenomic

cancer; cytostatic; carcinogen; pharmacodyanamic marker; gene; ss.

WO200160860-A2 Homo sapiens. 멍 S

230

217

2 ACCACGCGACACAC 15

Matches Query Match

Local

Similarity Conservative

100.08;

Score 14; Pred. No. 134 G;

13; 0

Length 320; Indels

0

Gaps

0

Pred. No. 50; Mismatches

Sequence 320

вP;

35

A; 97 C; 77.8%;

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CC type or tissue in which a given gene is expressed and to allow a compared to the abundance or expression level of a given gene in a cc determination of the abundance or expression level of a given gene in a cc garticular tissue or cell. The methods are useful for determining the cc similarity of a toxic response to one or more individual compounds. The cc likelihood that a compound or test agent will induce various specific cl pathologies such as those of the liver (liver necrosis, fatty liver conserved to the protein adduct formation or hepatitis), those of the kidney, cc disease, protein adduct formation or hepatitis), those of the kidney, cc heart, brain or testes, or other pathologies associated with at least one cf the toxins. The methods are also useful for predicting or elucidating cf the potential cellular pathways influenced, induced or modulated by the cc compound or test agent due to the similarity of the expression profile compared to the profile induced by a known toxin. The present sequence is that of a canine DNA sequence which was claimed for use during the cc production of a canine microarray of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention is related to a novel isolated canine nucleic acid sequences and the construction of canine microarrays containing a significant portion of the canine genome. The isolated canine nucleic acid sequences of the invention may be useful for drug screening and toxicity assays. The invention may be useful for assessing the impact, including toxicity, of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism. The methods are useful for detecting genes that are up- or down-regulated in canines in a disease state. The sequences are useful as diagnostic agents or markers to detect a cellular response in a sample individually or as part of a gene expression profile. It is also useful as a target for agents that modulate gene expression or activity. The database is useful for producing electronic Northerns that allow the user to determine the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid molecule, useful for drug screening and toxicity assays or for assessing the impact, including toxicity, of compound, pharmaceutical agent or environmental pollutant on a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 6234; 41pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-MAY-2002; 2002US-0377240P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                living organism.
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PFIZER PROD INC.
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RESULT 10
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Best Local S
Matches 14
17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cell carcinogenic potential of a compound; (d) assessing the aggressiveness or indolence of prostate cancer in a patient; (ii) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, use for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                                                                                                                                                                                   Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-2001
                                                                                                                              20-FEB-2001;
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                                                                                                                                                                                                                                                                                 Homo sapiens.
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                            2000US-0183319P.
2000US-0189862P.
2000US-0207454P.
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                                                                                                                                                                                                                                                                                                                                 cancer; cytostatic; carcinogen; pharmacodyanamic marker;
marker; gene; ss.
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Pred. No.
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29-NOV-2001

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24-MAY-2000; 2000US-0206690P 24-MAY-2001; 2001WO-US017076

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RESULT 11
ABN75645
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Best Local
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                                                                                                                                                                                             Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cancer has metastazized in a patient; (f) assessing the aggressiveness or indolence of prostate cancer in a patient; (ii) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABN75645;
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                                                                                                                                                 Homo
                                                                                                                                                                                 dermatological; analgesic; virucide; antibacterial; fungicide; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                       Human ORF592
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13-DEC-2000; 2000US-0255281P.
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                                                                                                                                                 sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plated nucleic acid molecule associated with cancerous state cells and correlating with presence of prostate cancer, uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACGCGACACACTT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 6811; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA, SEQ ID NO:1183.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC neurological disorders such as epilepsy and Alzheimer's disease.

CC cardiovascular diseases, immune system disorders, disorders related to corgan transplantation, disorders of tissue growth and regeneration, and cholesterol ester storage disease, and infectious diseases caused by viral, bacterial, corgan and other pathogens. ORFX nucleic acids may also be used as a corgan and other pathogens, in the detection of ORFX genomic sequences cor transcripts, in the identification and cloning of homologous corrections, in genetic diagnosis, and in forensic biology. The ORFX corcleic acids may additionally be used to produce transgenic animals conclude and in drug screening. The ORFX proteins may also be used as cimmunogens to generate specific antibodies, which are useful in the corgan activity of ORFX diagnosis, treatment and monitoring of ORFX-associated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC ABNY9587 represent CONAs encoding them. The invention also encompasses CC ABNY9587 represent collass and them. The invention also encompasses of collectively considered to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX CC polynucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX proteins, antibodies of ccivity, and methods of screening for modulators of ORFX expression or ccivity, and methods of screening individuals for a predisposition to an CC ORFX-associated disorder. The ORFX proteins of the invention have a wide crange of biological activities, such as cytokine, cell proliferation, cc cell differentiation, immune modulation, haematopoiesis regulation, cc tissue growth, angiogenesis, activity, thrombolytic activity, chemotactic/CC chemokinetic activity, haemostatic activity, thrombolytic activity, creceptor/ligand, antiinflammatory activity, thrombolytic activity, cand antiinfective activity, and behaviour. ORFX proteins, conclude acids and antibodies may be used in the treatment of cancers, cother proliferative disorders such as sporiasis and benign tumours, and altheing activity and behaviour. ORFX proteins, and activity disorders such as pooriasis and benign tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 561-562; 2508pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              designated ORF (open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplantation.
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                     Human; prostate pharmacogenomic
                                                                                         Human prostate expression marker cDNA 1395.
                                                                                                                                                                                                                                   ABV01404 standard; cDNA; 437
                                                                                                                                            13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 113 A; 121 C; 120
                                                                                                                                          (first entry
                          cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.8%;
                        cytostatic; carcinogen; pharmacodyanamic marker;
gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represent 4534 novel human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 14;
Pred No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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RESULT 13
ABV10573/c
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUN-2000;
18-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-2000;
25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 315; 11750pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-FEB-2000;
17-FEB-2000; 2000US-0183319P
                                                                                                                              Human; prostate pharmacogenomic
                                                                                                                                                                       Human prostate expression marker cDNA 10564.
                                                                                                                                                                                                                                                        ABV10573 standard; cDNA; 484
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                         20-FEB-2001; 2001WO-US005171.
                                                   23-AUG-2001
                                                                              WO200160860-A2
                                                                                                       Homo sapiens.
                                                                                                                                                                                                   13-SEP-2002
                                                                                                                                                                                                                                                                                                                         288
                                                                                                                                                                                                                                                                                                                                             4 CACGCGACACACTT
                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                         CACGCGÁCACACTT 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2000US-0183319P.
; 2000US-0189862P.
; 2000US-0207454P.
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0255281P
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2000US-0219007P.
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 128 A; 103
                                                                                                                                cancer; cytostatic; carcinogen; pharmacodyanamic marker;
marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                          100.0%; **
                                                                                                                                                                                                                                                                                                                                                                                                         77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
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Pred. No.
                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                   112 G;
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   91 T; 0
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RESULT 14
ABQ14948/c
ID ABQ149
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Best Local S
Matches 14
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25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                              Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, use for detecting presence of prostate cancer.
WPI; 2002-371829/40
                                                                             01-SEP-2000;
05-SEP-2000;
                                                                                                                                                                                                                                                                                                Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                               ABQ14948 standard;
                         Olek A,
                                                                                                                    01-SEP-2001; 2001WO-EP010074.
                                                                                                                                                 07-MAR-2002.
                                                                                                                                                                           WO200218632-A2
                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                           12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                    ABQ14948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
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                                                     EPIGENOMICS
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                         Piepenbrock
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2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
2000US-0255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                              2000DE-01044543
                                                                                           2000DE-01043826
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                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                               for detecting cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                               DNA;
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                         Berlin K,
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Pred. No.
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useful
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methylation of a particular cytosine in a motif 5'-CpG-3', present in a CG genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, CG of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the CG degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of coligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms CG (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method of content of the degree of cytosine methylation described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining the degree of cytosine diagnosis and prognosis, comprises
                                             determining the closure of the in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chemically treated DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            describes a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            method for determining the degree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  methylation in genomic DNA, selective hybridization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            German.
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밁 გ Matches Query Match Local 548 14; N Similarity ACCACGCGACACAC Conservative 77.8%; 535 15 <u>..</u> Score 14; DB 6; Pred. No. 49; Mismatches 0; Indels Length 732; 0 Gaps

0

Sequence 732 BP;

64

A; 82 C;

341 G;

245

T; 0 U; 0 Other;

disclosure of

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RESULT 15
ABQ14949
Oligonucleotide for
                                                                                   12-JUL-2002
                                                                                                ABQ14949
                                                                                                standard; DNA;
                                                                                   (first entry)
                                                                            detecting cytosine methylation
                                                                                                732
                                                                             SEQ
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SNP; cell differentiation; ds drug; side effect; cancer; central nervous system; card
gastrointestinal; respiratory system; single nucleotide Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;

Homo sapiens.

WO200218632-A2

07-MAR-2002

01-SEP-2001; 2001WO-EP010074

01-SEP-2000; 05-SEP-2000; 2000DE-01043826. 2000DE-01044543.

(EPIG-) EPIGENOMICS Ą

Olek A, Piepenbrock C, Berlin ᄌ Guetig Ö

WPI; 2002-371829/40.

Determining the degree of cytosine diagnosis and prognosis, comprises methylation in genomic DNA, selective hybridization of useful for

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PT from chemically treated DNA.

XX

XX

Claim 12; 56pp + Sequence Listing; 56pp; German.

XX

This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes, each with at least one member, CC degree of hybridisation to both classes is determined from the label on CC oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., CC particularly by detecting mutations or single nucleotide polymorphisms CC (SNP's); and (ii) for differentiation. The method allows the methylation cc investigating cell differentiation. The method allows the methylation cc status of many C residues to be determined simultaneously. ABO13410-CC ABD54121 represent genomic DNA sequences used to illustrate the method CC disclosure of the invention

XX Sequence 732 BP; 245 A; 341 C; 82 G; 64 T; 0 U; 0 Other;

Query Match

Poert I Ccal Cimilarity 100 0%. Pred No. 49:
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Maximum DB
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seq length: 2000000000
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18
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l: /cgn2_6/ptodata/1/pubpna
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Copyright (c) 1993 - 2005 Compugen Ltd.
                     / Cgn2_6/ptodata/1/pubpna/US09E PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09E PUBCOMB.seq:*
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/ Cgn2_6/ptodata/1/pubpna/US10E PUBCOMB.seq:*
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cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score	Query Match Length DB	Length	BB	ID	Description
1	18	100.0	18	ا و	US-09-872-051-11	Sequence 11, Appl
N	18	100.0	18	18	US-10-790-430-11	Sequence 11, Appl
ω	18	100.0	1183	9	US-09-872-051-8	Sequence 8, Appli
4.	18	100.0	1183	18	US-10-790-430-8	Sequence 8, App
U	16	88.9	1818	18	US-10-425-115-84576	Sequence 84576, A
o,	15	83.3	21	17	US-10-349-143-7605	Sequence 7605, Ap
c 7	15	83.3	445	18	US-10-357-930-19880	Sequence 19880, A
ი 8	15	83.3	500	18	US-10-357-930-49671	Sequence 49671, A
ი 9	15	83.3	533	13	US-10-027-632-234880	Sequence 234880,
c 10	15	83.3	533	17	US-10-027-632-234880	Sequence 234880,
11	15	83.3	641	18	US-10-767-701-6161	Sequence 6161, Ap

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e 14061	e 126, F	e 1024	e 8531,	æ	e 4526	10034	e 23957,	e 1100	e 25043	e 2504	e 38277	e 38277	e 23101	e 20475	e 20475	e 33608	36285		21630	403,	36207	20494,		e 5342,	26676,	e 15388,	e 15466	e 3197,	Sequence 3196, Ap	e 5457,	e 823,	e 8948,	13,

# ALIGNMENTS

US-09-872-051-11

GENERAL INFORMATION:

APPLICANT: Monsanto Co APPLICANT: Behr, Carl Sequence 11, Application US/09872051 Patent No. US20020013960A1

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APPLICANT: Hironaka, Catherine
APPLICANT: Heck, Gregory

APPLICANT: You, Jinsong

TITLE OF INVENTION: Corn Event pv-ZMGT32(nk603) and Composition and Methods for Detailt Detailt.

TITLE OF INVENTION: Thereof

FILE REFERENCE: 38-21 (52258) B

CURRENT EPILING DATE: 2001-06-01

PRIOR APPLICATION NUMBER: 60/213,567

PRIOR APPLICATION NUMBER: 60/213,567

PRIOR FILING DATE: 2000-06-22

PRIOR APPLICATION NUMBER: 60/241,215

PRIOR APPLICATION NUMBER: 60/241,215

PRIOR FILING DATE: 2000-10-13

NUMBER OF SEQ ID NUMBER: 60/240,014

PRIOR FILING DATE: 2000-10-13

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3.0

SEQ ID NO 11

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: SOURCE

OTHER INFORMATION: Zea maize genomic DNA and vector DNA

US-09-872-051-11

Query Match

100.0%: Score 18; DB 9; Length 18;
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100.0%;

Pred. No. 0.97;

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CURRENT FILING DATE: 2004-03-01
PRIOR APPLICATION NUMBER: US/09/872,051
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 2000-10-13
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Matches 18
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                                                                               APPLICANT: Heck, Gregory
APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Detec
TITLE OF INVENTION: Thereof
FILE REFERENCE: 38-21(52258)B
CURRENT APPLICATION NUMBER: US/09/872,051
CURRENT APPLICATION NUMBER: US/09/872,051
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
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APPLICANT: Behr, Carl
APPLICANT: Hironaka, (
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APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Detec
TITLE OF INVENTION: Thereof
FILE REFERENCE: 38-21(52258)B
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NUMBER OF SEQ ID NOS: 16
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OTHER INFORMATION: Zea maize genomic DNA and vector DNA
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NAME/KEY: source
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                  APPLICATION NUMBER: 60/241,215
FILING DATE: 2000-10-13
APPLICATION NUMBER: 60/240,014
FILING DATE:
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5. US20020013960A1
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Hironaka, Catherine
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Matches 1
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LENGTH:
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                                                                       Matches
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Best Local Similarity
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PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/240,014
PRIOR FILING DATE: 2000-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 38-21(52258)B
CURRENT APPLICATION NUMBER: US/10/790,430
CURRENT FILING DATE: 2004-03-01
PRIOR APPLICATION NUMBER: US/09/872,051
PRIOR FILING DATE: 2001-06-01
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                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: source
LOCATION: (1)..(1183)
OTHER INFORMATION: 1-164 Agrobacterium tumefaciens nos 3' terminator
OTHER INFORMATION: 185-381 construct vector DNA
OTHER INFORMATION: 382-686 Zea maize plastid genes, rps11 and rpoA
OTHER INFORMATION: 687-1183 Zea maize genomic DNA
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NAME/KEY: source
LOCATION: (1)..(1183)
CTHER INFORMATION: 1-164 Agrobacterium tumefaciens n
OTHER INFORMATION: 165-381 construct vector DNA
OTHER INFORMATION: 382-686 Zea maize plastid genes,
OTHER INFORMATION: 687-1183 Zea maize genomic DNA
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                       TGCTGTTCTGCTGACTTT 18
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                                                                       Conservative
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                                                                                        100.0%; Score 18; DB 18; Length 1183; 100.0%; Pred. No. 0.88;
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RESULT 5 US-10-425-115-84576

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PRIOR APPLICATION NUMBER: US/05/422,978

PRIOR FILING DATE: 1999-10-20

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

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US-10-425-115-84576
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LENGTH: 1818
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Best Local
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Publication No. US20040214272A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
FURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
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APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
                                                                               Matches
                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OLIVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT FILING DATE: 2003-01-21
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NAME/KEY: unsure
LOCATION: (1)..(1818)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                             NAME/KEY: primer_bind
LOCATION: 1..21
OTHER INFORMATION: upstream amplification primer 99-9623 for SEQ 3671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo Sapiens
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                                                                                                  Similarity
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                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daniel
                                                                        83.3%; >--
100.0%; Pr
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                                                                                                Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                   Mismatches
                                                                                                                       DB 17; Length 21;
                                                                                                    49;
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                                                                                   Indels
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                                                                                   Gaps
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US-10-357-930-19880/c
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                                                          CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/201,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-05-09
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PRIOR FILING DATE: 2000-03-16
PRIOR PELICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 49671, Application US/10357930 Publication No. US20040259086A1
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Best Local (
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LENGTH: 445
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APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS,
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
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CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
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TITLE OF INVENTION: NOVEL GENES, COMPOSITION
TITLE OF INVENTION: IDENTIFICATION, ASSESS
TITLE OF INVENTION: HUMAN PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
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PRIOR FILING DATE: 2000-12-13
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PRIOR FILING DATE: 2000-02-17
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                                            APPLICATION NUMBER: 60/219,007
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60/255,281
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-49671
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                                                                                                                                                                                                                                                                                     RESULT 10
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US-10-027-632-234880
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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Best Local S
Matches 15
                                                                                                               GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 234880
LENGTH: 533
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49671
                                                                                                                                                                                                               Sequence 234880, Application US/10027632 Publication No. US20030204075A9
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Best Local Similarity
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FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-12-13
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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100.0%; Pred. No.
ative 0; Mismatc
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                                                                                                                   and Mapping of Single Nucleotide in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 46;
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; ORGANISM: Human
US-10-027-632-234880
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                             Sequence 77613, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 6161
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APPLICANT:
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT FILING DATE: 2004-01-29
NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
              APPLICANT: Cao Yongwei TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
                                                                                                                    APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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CURRENT APPLICATION NUMBER: US/10/424,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 641
TYPE: DNA
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                           586 TGCTGTTCTGCTGAC
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100.0%; Pred. No.
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_41100C.1
US-10-424-599-77613
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US-09-764-891-8948
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US-10-322-281-823
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US-09-764-891-8948
                                                                                                                                              ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-322-281-823
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Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
DEFINE TOWNSTAND ASTRONOMY.
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SEQ ID NO 77613
LENGTH: 695
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NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8948
LENGTH: 3167
TYPE: DNA
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                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FRANKSEQ for Windows Version 4.0
SEQ ID NO 823
LENGTH: 70019
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 823, Application US/10322281 Publication No. US20040126762A1 GENERAL INFORMATION:
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Best Local S
                                                                     Query Match 83.3%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 41 Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                               APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001000
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ORGANISM: Glycine max
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Local Similarity 100.0%; Pred. No.
hes 15; Conservative 0; Mismatc
 27137 TGTTCTGCTGACTTT 27151
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                         TGTTCTGCTGACTTT 18
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44;
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TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preville REFERRENCE: and treatment of infection FILE REFERENCE: 9710-003-999; CURRENT APPLICATION NUMBER: US/10/289,762; CURRENT FILING DATE: 2003-03-27; NUMBER OF SEQ ID NO 5457; CURRENTED NA ORGANISM: Chlamydia pneumoniae
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Publication No. US20040006218A1
GENERAL INFORMATION:
APPLICANT: Griffals, R.
                                                                                              Query Match
Best Local 9
                                                                               Matches
16 GTTCTGCTGACTTT 3
                           5 GTTCTGCTGACTTT 18
                                                                               Similarity 100.0%; 14; Conservative 0;
                                                                                 77.8%; Score 14; DB 100.0%; Pred. No. 1.8 ive 0; Mismatches
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Search completed: February 9, 2005, 11:12:46
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seq length: 2000000000
100.0 18
100.0 1183
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100.0 232994
94.4 118174
94.4 175940
98.9 719
88.9 42563
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Gapop_60.0 , Gapext 60.0
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Match Length
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AC13925

AC133551

AX160838

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# ALIGNMENTS

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RESULT 2 AX342369 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	Db Oy	Query Match Best Local Matches 1	JOURNAL FEATURES SOURCE	KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	RESULT 1 AX342373 LOCUS DEFINITION ACCESSION VERSION
AX342369 1183 bp DNA linear Sequence 8 from Patent EP1167531. AX342369 AX342369.1 GI:18151812	1 ACCAAGCTTTTATAATAG 18                   1 ACCAAGCTTTTATAATAG 18	Match 100.0%; Score 18; DB 6; Length 18; Local Similarity 100.0%; Pred. No. 16; les 18; Conservative 0; Mismatches 0; Indels	for detection thereor Patent: Ep 1167531-A 12 02-JAN-2002; Monsanto Technology LLC (US) Location/Qualifiers 118 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Agrobacterium tumefaciens nos 3' rice actin promot er DN"	synthetic construct synthetic construct other sequences; artificial sequences.  1 Behr, C.F., Hironaka, C., Heck, G.R. and You, J. Corn transformant pv_zmgt32 (nk603) and compositions	AX342373 18 bp DNA linear Sequence 12 from Patent EP1167531. AX342373 AX342373.1 GI:18151816
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RESULT 3
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RS Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Bandaranaike, D., Barber, M., Barastead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Biswalo, K., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Deramo, C., Ding, Y., Dinh, H., Divya, K., Davila, M.L., Davils, C., Davy, Carrell, D., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Gebregoorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Guvara, W., Harrandez, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, M., Hernandez, J., Hernandez, S., Hladun, S.L., Hodgson, A., Hopues, M., Jackson, L., Jackson, L., Jackson, L., Jang, H., Johnson, B., Johnson, R., Johnson, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156
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Corn transformant pv_zmgt32 (nk603) and compositions and methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
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AC106676.4 GI:30578541
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Monsanto Technology LLC (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for detection thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCAAGCTTTTATAATAG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 225438)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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CH230-107N12, WORKING DRAFT SEQUENCE, 3
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REFERENCE
AUTHORS
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Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:23268058.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs within a contigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley,K.C.
Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 225438)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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REFERENCE AUTHORS TITLE

JOURNAL

TITLE

JOURNAL

COMMENT

JOURNAL

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are unknown.

* This record will be updated with the finished sequence Center project name: GLUL Center clone name: CH220-107N12 Center clone name: CH220-107N12 Center Summary Statistics Assembly program: Atlas 3.0; Consensus quality: 201968 bases at least Q40 Consensus quality: 205320 bases at least Q30 Consensus quality: 207760 bases at least Q20 Estimated insert size: 213439; sum-of-contigs estimation Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu ------Project Information Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

be preserved.

222661 222761

as soon as it is available and the accession number will

222660: contig of 222660 bp in length 222760: gap of unknown length 224015: contig of 1255 bp in length

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SOURCE
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AC110467
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Best Local Similarity
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      Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Bader, H., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Bader, H., Bardarinanike, D., Barber, M., Barcastead, M., Benahmed, F., Badwin, D., Baddarinanike, D., Barber, M., Barter, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Coyle, M., Cree, A., D'Souza, L., Coyle, M., Chen, Y., Chen, Z., Chu, J., Checkell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Chelgado, O., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotco, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Farser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebrageorgis, E., Geer, K., Gill, R., Gracia, A., Garner, T., Garza, M., Gebrageorgis, E., Geer, K., Gill, R., Gracia, A., Garner, T., Garza, M., Gubrarathe, P., Haaland, W., Hamilton, C., Hamilton, C., Hamilton, K., Harten, J., Hodson, A., Hoguer, M., Hollins, B., Howells, S., Hladun, S. L., Hodgson, A., Hoguer, M., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Kowis, C., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Li, Z., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Loudon, P., Longacre, S., Lopez, J., Longacre, S., Lopez, J., Mandum, B., Mastin, K., Martin, K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC110467 232994 bp DNA linear HTG 19-SEP-2002
Rattus norvegicus clone CH230-320D17, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC110467.4 GI:23195262
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complement(2211111...221919)
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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Martin, K., Martin, R., Martinez, E.
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Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfamkoch, C.,
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Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Rutz, S.J.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Sned, A., Sodergren, E., Song, X., Sitter, C.D., Smajs, D.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Weil, X., White, F.,
Wang, Q., Wang, S., Warren, J., Warren, R., Weil, X., White, F.,
Williams, G., Willson, R., Wleczyk, R., Wooden, H., Woorley, K.,
Wright, D., Waldron, J., Zhou, J., Zhou, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
Submitted (19-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 19, 2002 this sequence version replaced gi:21741421. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bem.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-FEB-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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COMMENT

Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu Center: Baylor College of Medicine

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved. 152447 152547 152446: contig of 152446 bp in length 152546: gap of unknown length 214193: contig of 61647 bp in length

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Submitted (04-SEP-2004) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
OK 73019, USA
ON Sep 4, 2004 this sequence version replaced gi:51699588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shaull,S., Lin,S., Dixon,R., May,G., Sum Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone mth2-17p13
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------- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
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Submitted (10-DEC-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 118174)
Shaull, S., Lin, S., Dixon, R.,
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Medicago truncatula (barrel medic)
Medicago truncatula
                                                                                                                           Center code: UOKNOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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AC138014.30 GI:51889812
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Medicago truncatula clone mth2-17p13, WORKING
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCAAGCTTTATATATAG 83220
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'db_xref="taxon:10116"
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215380: contig of 1087 bp in length
215480: gap of unknown length
217850: contig of 2370 bp in length
217950: gap of unknown length
218965: contig of 1015 bp in length
218965: gap of unknown length
220974: contig of 1909 bp in length
221074: gap of unknown length
232994: contig of 11920 bp in length.
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                                                                                                                                                                                                                                                                                                                                Sumner, L., Gonzales, B
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SEQUENCE, 3
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(CE 1 (bases 1 to 154559)

RES Hillier, L.W., Fulton, R.S., Fulton, L.A., Graves, T.A., Pepin, K.H., Wagner-McPherson, C., Layman, D., Maas, J., Jaeger, S., Walker, R., Wylie, K., Sekhon, M., Becker, M.C., O'Laughlin, M.D., Schaller, M.E., Fewell, G.A., Delehaunty, K.D., Miner, T.L., Nash, W.E., Cordes, M., Pewell, G.A., Delehaunty, K.D., Miner, T.L., Lamar, B., Courtney, L., Kalicki, J., Ozersky, P., Bielicki, L., Scott, K., Holmes, A., Harris, A., Strong, C.M., Hou, S., Tomlinson, C., Harkins, R., Harris, A., Strong, C.M., Hou, S., Tomlinson, C., Harkins, R., Harris, A., Strong, C.M., Leonard, S., Rohlfing, T., Rock, S.M., Tin-Wollam, A.M., Abbott, A., Minx, P., Maupin, R., Strowmatt, C., Latreille, P., Miller, N., Johnson, D., Murray, J., Woessner, J.P., Wendl, M.C., Yang, S.P., Schultz, B.R., Wallis, J.W., Spieth, J., Bieri, T.A., Nelson, J.O., Berkowicz, N., Wohldmann, P.E., Cook, L.L., Hickenbotham, M.T., Eldred, J., Williams, D., Bedell, J.A., Mardis, E.R., Clifton, S.W., Chissoe, S.L., Warra, M.A., Raymond, C., Haugen, E., Gillett, W., Zhou, Y., James, R., Phelps, K., Iadanoto, S., Bubb, K., Sama, E., Levy, R., Clendenning, J., Kaul, R., Kent, W.J., Bork, P., Suyama, M., Bailey, J.A., Portnoy, M.E., Torrents, D., Chinwalla, A.T., Gish, M.R., Eddy, S.R., McPharson, J.D., Olson, M.V., Eichler, E., Green, E.D., Watterston, R.H. and Wilson, R.K.

All Nature 424 (4645) 157-164 (7001)
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Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens PAC clone
AC004925
AC004925.1 GI:4156174
                                                   Direct Submission
                                                                         Waterston, R.H.
                                                                                                                             The sequence of Homo sapiens Unpublished (2001)
                                                                                                                                                                                   2 (bases 1 to 154959)
Jones, K., Keppler, D. a.
                                                                                                                                                                                                                                                                                           Nature 424 (6945), 157-164 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by the finished sequence as soon as it is available the accession number will be preserved.

1 78995: contig of 78995 bp in length 78996 79095: gap of unknown length 84865 84964: gap of unknown length 84865 118174: contig of 33210 bp in length.
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This sequence will be replaced
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                                                                                                       (bases 1 to 154959)
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/mol type="genomic DNA"
/db_xref="taxon:3880"
/clome="mth2-17p13"
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                                                                                                                                                              and Tin-Wollam, A. sapiens PAC clone RP5-907C10
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Pred. No. 20;
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RP5-907C10
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     St. Louis
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NEIGHBORING SEQUENCE INFORMATION: Actual start of this clone is at base position 1 of RP5-907C10 actual end is at 154959 of RP5-907C10.	about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu source INFORMATION: This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at http://www.chori.org using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor. The clone may be obtained edonor. The clone may be obtained edonor. The tlone may be obtained enter from Genome Systems, Inc. (http://www.resgen.com); or from Pieter de Jong. VECTOR: pCYPAC2	This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.  MAPPING INFORMATION: The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center: For additional information	Web site: http://genome.wustl.edu Contact: sapiens@wastson.wustl.edu Center project name: H_DJ0907C10 Center project name: H_DJ0907C10  NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.	to 154959)  ission 30-JAN-2004) Department of Genetics, Washingto 30-JAN-2004) Department of Genetics, Washingto 4444 Forest Park Avenue, St. Louis, Missouri 1999 this sequence version replaced gi:3213077 Genome Center Washington University Genome Sequencing Center code: WUGSC	6 (bases 1 to 154959) Waterston,R. Direct Submission Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA 7 (bases 1 to 154959) Waterston,R. Direct Submission Submitted (26-APR-2003) Department of Genetics, Washington Submitted (26-APR-2003) Department of Genetics, Missouri 63108, USA University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA	MO 63108, USA 4 (bases 1 to 154959) Waterston,R.H. Direct Submission Submitted (14-JAN-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 154959) Waterston,R. Direct Submission Submitted (22-JAN-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
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96167 .9810 7 /rpt_family="L1" 98347 .9908	SJ44 585   Family="Alu"	/codon_start=3 /product="unknown" /product="unknown" /product="unknown" /product="unknown" /product="unknown" /protein_id="AAD08852.1" /db_xref="g1.4176376" /tb_xref="g1.4176376" /tb_xref="g1.4176376" /tb_xref="g1.4176376" /tb_xref="g1.4176376" /tb_xref="g1.4176376" /tb_xref="g1.4176376" /tb_xref="g1.4176376" /tb_xref="g1.4176376" /tb_xref="g1.4176376" /tb_f="g1.4176" /tb_f="g1.4	join(28142870,68497005,86348839,1439814533, 2047020558,2250722598,2445524560,2573825891) /gene="pCT1" join(<28142870,68497005,86348839,1439814533, 2047020558,2250722598,2445524560,2573825850) /gene="pCT1" /note="Homo sapiens, clone MGC:10280 IMAGE:395573, mRNA complete cds.; H_DJ0907C10.4 This gene was based on gj(12804138 13123773) Continues from H_NH0563L14.1"	/rpt_family="L1" 2297.	1128. 1429 /rpt_family="Alu" 1554. 1648 /rpt_family="L1" 1659. 1786 /rpt_family="L1" 1790. 1916 /rpt_family="L1" 1790. 1916 /rpt_family="L1" 1790. 2296	Location/Qualifiers  1. 154959 /organism="Homo sapiens" /mol type="genomic DNA" /db_xref="taxon:9606" /chromosome="7" /chromosome="7" /clone="RP5-907C10" /clone="RP5-907C10" /clone lib="RPCI-5" 68

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REFERENCE
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VERSION
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                                                                                                                                                                                                                                                                                The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             requests: clonerequest@sanger.ac.uk
On Jul 23, 2000 this sequence version replaced gi:9367364.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submist sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
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175940 bp DNA linear PRI 21-AUG-Human DNA sequence from clone RPI1-57G10 on chromosome 10 Conte a J-domain containing protein (JDP1) isoform B, the SIRT1 gene (Sir2-like proteins (siruitins) type 1), part of a novel gene (Sir2-like proteins) type 1), part of a novel gene similar to KIAA0033, two ribosomal pseudogenes, 2 CpG islands, RSTES care and GCSC.
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                                                                                                                                                                         Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                         RP11-57G10 is from the library RPCI-11.1 constructed at the Roswell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (21-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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AL133551.13 GI:9407715
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                                                                                                                                                                    VECTOR: pBACe3
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                                                                                                                                         sequence is the entire insert of clone RP11-57G10 The true
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                                                                                                               end of clone RP11-474D14 is at 172652 in this sequence
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10420. .10528
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9941. .10129
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                                                                            Location/Qualifiers
'mol_type="genomic DNA"
                             organism="Homo sapiens"
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3. .10907
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/note="MIR repeat: matches 76. .146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8908. .9107
/note="MER7A repeat: matches 1.
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/note="MER7A repeat:
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/note="MLT2CB repeat: matches 42.
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/note="MLT1F repeat:
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/note="LIMA4 repeat: matches 5704. .6298 of consensus"
                                                                                                                                                                                                                    /note≃"AluSq repeat: matches 1.
complement(14553. .14948)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          10489. .10938
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/note="MLT2A repeat: matches 1.
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11938. .12442
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                /note="L2 repeat: matches 1843.
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/chromosome="10"
                                                    'note="AluJb repeat: matches 1.
                                                                                        'note="AluSx repeat: matches 1.
                                                                                                                            note="MLT1J repeat: matches 113.
                                                                                                                                                                                                     note="match: GSS: Em:AQ113044"
                                                                                                                                                                                                                                                                                            /note="AluY repeat: matches 1. .303 of
l3888. .13947
                                                                                                                                                                                                                                                                                                                                                                evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluY repeat:
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   8101. .18225
                                                                                                                                                                                                                                                                         note="MLT1J repeat: matches 453.
                                                                                                                                                                                                                                                                                                                                               note="tRNA-Ser-TCA repeat: matches 8.
                                                                                                                                                                                                                                                                                                                                                                                                     'note="CpG island"
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                                                                                                                                                                                                                                                            .14387
                                   .18107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Alu repeat: matches 238. .306 of consensus"
27063. .27175
/note="AluJo/FRAM repeat: matches 144. .250 of consensus"
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27004. .27072
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25153..ehluJo repeat: matches 1..263 of consensus" 25420..25432
/note="FLAM A repeat: matches 120..133 of consensus 26638..26802
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/note="LTR33 1
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/note="match: GSS: Em:AQ627100"
19338. .19830
/note="AluSx repeat: matches 1. .294 of consensus"
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                                                             /note="MER5A repeat: matches 34300 .34598
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/note="L2 repeat: matches 2476.
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/note="AluJo repeat:
33377. .33567
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32163. .32593
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/note="MLTIC repeat: matches 1.
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                                                note="MLTIA1 repeat: matches 93.
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Uncultured bacterium clone COB
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                                                                                                 Arabidopsis thaliana (thale cress)
Kaneko, T.,
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                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                  88.9%; Score 16; DB 1; Lilarity 100.0%; Pred. No. 1.3e+02; Conservative 0; Mismatches 0;
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35183. .35482
/note="AluSq repeat: matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="uncurrunt"
/mol_type="genomic_DNA"
/isolation_source="termite_intestinal_tract"
/isolation_source="termes orthognathus, soi
                                                                                                                                                                                                                                                                                                                                                                                                                       /product="16S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     environmental_sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="COB P1-13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="uncultured
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   Katoh, T.,
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   Sato,S.,
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DNA,
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P1-13 16S
     Nakamura,Y.,
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19;
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      Asamizu, E.,
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ne 5, TAC clone:K19M13.
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      Kotani, H.,
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                                                                           CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL Submitted (06-OCT-1998) Yasukazu Nakamura, Kazusa DNA Research Instituted, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)

Address for correspondence: kaos@kazusa.or.jp, Address for correspondence: kaos@kazusa.or.jp, Address for correspondence: kaos@kazusa.or.jp, Passe see http://www.kazusa.or.jp/kaos@cgi-bin/agd_graph.cgi?c=K19M13

Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html), MerGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brende1, Stanford University, http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).

Genes encoding tRNAs are predicted by tRNAscan-SE/).

This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is T32G24 and the 3' clone is MQM1.

S Location/Qualifiers

1. 42563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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/translation="MVLLGLLGDWETKHEMESVEDPSKEKPSWRILNVPGKPPKLAWG HSTCVVGGTRVLVLGGHNGEEWILNELHELCLASWQDSDL" complement(join(10326. 10490,10573. 10656,10748. 110792,10888. 10942,11028. 11147,11224. 11313,11604. 11725) /note="unnamed protein product; gene_id:K19M13.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLTSLQLSGNKFIGHIPASITGLQNLWSLNLSRNLFSDPLPVVGARGFPSLLSIDLSY
NNLNLGAIPSWIRDKQLSDINLAGCKLRGTFPKLTRPTTLTSLDLSDNFLTGDVSAFL
TSLTNVQKVKLSKNQLRPDLSKLKLPEGVASIDLSSNLVTGSLSSLINNKTSSFLEBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIIEDTTGVLDSWVGKDCCNGDWEGVQCNPATGKVTGLVLQSAVNEPTLYMKGTLSPS
LGNLRSLELLLITGNKFITGS INSFSNITSLRQLILDNSLQCNVLSSLGHLPLLEI
LSLAGNRFSGLVPASFGSLRRLTMILARNSFSGPIPVTFKNILKLENLLSSNLLSG
PIPDFIGQFQNLTNLYLSSNRFSGVLPVSVYSLRKLQTMSLERNGLTGPLSDRFSYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                      HLTNNQISGRI ÞÐFGESLNLKVLNIGSNKI SGQI ÞSSI SNLVELVRLÐI SRNHI TGGI
ÞQAI GQLAQLKWLÐLS I NALTGRI ÞÐSLLNI KTI KHAS FRANRLCGQI ÞQGR ÞFNI FÞ
                                                                                                                                                                                                                                                                                                                                                              complement (join (7408.
                                                                                                                                                                                                                                                                                                                                                                                                AAAYLHNLCLCGKPLPACRKTMK"
                                                                                                                                                                                                                                                                                                   /note="unnamed protein unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
/product="disease resistance protein-like"
/protein_id="BAB09556.1"
                                                                                                                                                                                                   /evidence=not_experimental
/protein_id="BAB09557.1"
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mol type="genomic DNA"

/db_xref="taxon:3702"

/chromosome="5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MQNLKWVLMNLLFVSALVRNFVLSSSQQVICSSQDRATLLGFKS
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                                                                                                                                                                                                                                                                                                                                  product;
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SdC

QDPPTRCSWGNTGGQDREDISSTVSDPGPIWDAGPKWDTEPSAWDVENSIELPGPPED

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/evidence=not experimental
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VKFWDLETFELI GSGGEETAGVRCLSENPDGKTVLCGLQESLKI FSWEPIRCHDGVDV
GWSRLSDMNVHEGKLLGCSYNQSCVGVWVDLSVFLSPYISFSFCLI VAĞSKLYEPTH
FQWHGQRTEPCWAGDTAQSWGHFEKRSCSGRDDVVLMDNNSKTVLGKLSVSQNVDPLL
KETKSLGRLSVSQNSDPSTKETKSIGRSSTSQNSESSMKESKPLGRLSVSQNVDPLL
KETKSLGRLSVSQNSDPSTKETKSIGRSSTSQNSESSMKESKPLGRLSVSQNVDPLL
KETKSLGRLSVSQNSDPSTKETKSIGRSSTSQNSESSMKESKPLGRLSVSQNSDVSKE
SKTTSSSTGSLEGTTHRVSSTNVSKATSGVSTAVSMAATSRKHETKAMPKANPVNKAAD
FAPVIVPRADPRIEQATESPABLDIIATMYSLQAADSRRSPSSRNSNSRSVLE
MSESQPVERNNIPDGGTLDGGKVGMRGATERSINDFRYKRYGRSNSRSRMGSPFNHD
ENVLDLVSHRSNRDDSPTESQKGGDSSAQLSSFLQMKRISFMCLIIGSRFGSLVINEE
RRGRESNFESGPVSNFSSGMMPAPNIR PSMMFKRGMHMPVEQGIDSPSEENIVEDIMG
KHNGPVSSMQSRLAKLQVVRKYWERNDVKNSIGSIEKMADNAVTADVLGIITENDELL
TLDNCTSLLPLLTALLGSGMDQHLSVSLDLLLKLVRLYGSPIYSSLSAPASVGVDIEA
EQRIERYSRCFVELEKVKACLPSLASISGSFIIITMSLTTLDKNAEQKPVFLVEEPAS
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gb|AAB71474.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="unnamed protein product; gene_id:K19M13.8
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(26890. .27881,28441. .28540,2866)
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PLSLFTSQSQIKHSSSRKTSRTTIRCDVAIKSADSINADANPSSSPSSEEEIEAEAKA
KIGSRVRVTAPLKVYHVNRVPEVDLEGMEGKLKDYVAVWKGKRISANLPYKIEFFKEI
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/note="unnamed protein product; contains similarity to
ferredoxin-thioredoxin reductase variable chain
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AIGKPNAILVSSRVLVCCQSLYGHSSGIDSVTFDASEVLVAAGAASGTIKLMDLEEAK
IVRTLTGHRSNCISVDFHPFGEFFASGSLDTNLKIMDIRKKGCIHTYKGHTRGVNVLR
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PLTAFFIFMSDFRKTFKSEHNGSLAKDAAKIGGEKWKSLTEEEKKVYLDKAAELKAEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown protein"
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/protein_id="BAB09560.1"
/db_xref="GI:9759082"
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RESULT 10
AF467900/c
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Best Local
JOURNAL
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                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Amygdaloldeae; Prunus.
                                                                                                                                                                                                                                                                                                                                                                                                     AR467900 48843 bp DNA linear PL Prunus persica clone pPn31C7 hypothetical proteins, an hypothetical transcription factor genes, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
16; Conser
                                                                    Georgi,L., Wang,Y., Yvergniaux,D., Ormsbee,T., Inigo,M., Reighard,G. and Abbott,G.
Construction of a BAC library and its application to the identification of simple sequence repeats in peach [Prun
                                                                                                                                                                                                                                                                             Prunus
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Theor. Appl. Genet.
12582893
                                                 (L.) Batsch
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syylkdvttsslsdddfsqeeceelhgrinngfakrltvvdweekarslhedvtkyl
ekrellonddegkrlvdeveivaelegecedddddtiebekarslhedvtkyl
ekrellonddegkrlvdeveivaelegecedddddbriebefydddeg
RQRDLFVSSSVKKSQERSLLLKWBEEQLRLLCOVPDVVASKLEPEFVDDDGKLVMDVP
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EPPANGITLNTDSITEGEMNTKVSQHQSSTPVIDLSNKTQAHSNPIEIIELSDDDDDD
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unknown protein"
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TTVDNfegrspdylykgmqmsnealgftkglisqtsmledkklhlvldldqtlihtik
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GGYDYARLVLEMIDPDKFyfGNRVITRRESPGFKTLDLVLADERGIVIVDDTSSVWPH
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GLKLRDRHEERGFTSPQSRLTVADRNFCGVPVNPTWRLNVMTRGLRTTRSLHVLDTKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join (37928. .38528,38657. .38766,39049. .39108,
39675. .40085,40152. .40239,40345. .40769)
/note="unnamed protein product; emb|CAB62634.1
yene_id:K19M13.11
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/protein_id="BAB09562.1"
/db_xref="GI:9759084"
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/db_xref="GI:9759086"
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AUTHORS
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Georgi, L.L., Wang, Y. and Abbott, A.G.
Direct Submission
Submitted (11-JAN-2002) Genetics and Biochemistry, Clemson
University, 122 Long Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MGMGVRNALICTHVISRPSLIFKISVKLFLLEESPSQVGLSAQD HLQAKASWLSHSSGTGSDDILPPGFEGAYSANQLQINVSQIPLIKHCPPRVVLNFTW QVCCGESKEVEIQNQREIFVLEAVYPRPSALPLNESVLADVEDSGHNUPPUPIT SIEDEDVGVDTSSASMAPFNIHTSTQSFLSVQIAAPSQSVVPNNRHHPTSNKEVAGIPVGVEDVVAAASAARGAIVNSNEHEMNIDHEILLIKILSNPKMIEKLYKDPQPMTRPP QMSIADPPPVHINRTESSSTESSTALSSGHFYPQPNVAGMGRFPDARPPPHAAISVPSPAVGPPPAKDINYYKSLIQQHGGDHDSFPFGNRHSDHSALNQESNNGYKSBDSKPPAVGPPPAKDINYYKSLIQQHGGDHDSFPFGNRHSDHSALNQESNNGYKSBDSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_type=inverted
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join(3833. .3907,4079. .4288,4418. .4542,4630.
/note="similar to hypothetical protein F6F9.9
Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_type=inverted
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                                                                                 /tranelation="MGASTSTEQKVSIEQREAEALAASTGALSMLQKSFSSLAHPDSN
AIPLNSLQQCFSLTHKNPVCEALTVPDSFPMLLDHLGSSILDLET SEKGGVSWVEFV
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LLMMCWAISMNSKTSKISKKTDLPLPDINQIVLSALVSCADVGSGLNVMDCQLSGLE
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SHLLSSGMAMAISLALRGTISEEISKVCFPSETDGIDKNLLYRSSLHGRGLNRFWSNI
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complement(join(7784. .7882,7973. .8098,8313.
8627. .8865,9253. .9440,9712. .10323,10419. .1
/note="similar to unknown protein MIJ24.8 in I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (join (<7784. . 7882, 7973. 8627. . 8865, 9253. . 9440, 9712. . 103
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join(<6350. .6706,7104. .>7133)
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/clone lib="pBeloBAC11"
/note="derived from genomic DNA partially digested with/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:3760"
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                                       EGYQGPLLMLFSATSGDASDGRANERKWTVGALTNQGFENKDLFYGSSGNLYAISPVF
HVYPPTGKEKNFVYSHLHPTGRTYEPKPKPVGIGFGGSLGNERIFIDEDFSKVTIRHH
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/db_xref="GI:27450531"
                                                                                                                                                                                                                                                                                                                                            thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVIIPAEELHQPAPGTKPRKADEKKQ"
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/product="hypothetical protein"
/protein_id="AAO14624.1"
/db_xref="GI:27450529"
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/mol_type="genomic DNA"
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join(6350. .6706,7104. .7133)
             aadktyopgslfpdogflpvealisevevwglggrsakdvodsykkreolftdorrkv
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.10323,10419. .>:
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3 CAAGCTTTTATAATAG 18
                                                                                        Similarity
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/note="likely the remains of a retroelement"
                                                                                                                                                                                                                                                                                                /note="likely the remains of a retroelement" 41144. .41437
                                                                                                                                                                                                                                                                                                                                                                                                                           RCIRILSPTEVQQMSEEGIKLLNSAAMQGINGTMSEGGRT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGSGVSAVIDPSVSSTILDEFSTLKNADFHNPSDCLLGNLSSSQDLQSQITSASLGDS
QAFSRQDLADNSGGTSSSNIDLDESSLLQNNGSWHQVVPPVRTYTKVQKTGSVGRSID
VTSFKNYEELCSAIECWFGLEGLLNDPRGSGWKLVYVDYENDVLLVGDDPWEEFVGCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKLAAGFYSFYNLYNQLTFANQNGSAAQLQTSFRPMQPPLESLLYHSQQTDMPNSDFN
STNGSLPFLDNDECIFYQSYQPFAGTLRSQGPLSVFGLQDSSAVLTEANNSSLTSIGQ
EMMDNSLNNCRLLPQVDQLTSSHQGPGSLNCISNSSSLRDLSDESNNQSGIYGCPNVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGTI VSTSDLDPLAMPGSKWANLQVEWDEPGCCDKQNRVSSWEIETPENIF I IPPSLTS
SLKR PSHTGFIGAETEWGNLI KRPFIR VEELIGNGUS FPYSISUNLCSEQLVNMLLKPQL
VNHAGTLAALQQQS PANGDLI ADMKAMQAKLI QKUPGVFSEGTTSLQSQUPADLISEGLUS
ATI DVNTTSHA I LPGKLNNLTKFGSQAPVGNSTDKTKLETDFSADQLSQLNSTGLGIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGGFSVPRRAAEKLFPPLDFTMQPPSQELVVRDLHDNSWTFRHIYRGQPKRHLLTTGW
SLFVGAKRLRAGDSVLFIRDEKSQLMIGVRRANRQQTTLPSSVLSADSMHIGVLAAAA
HAAANRSPFTIFYNPRACPSEFVIPLATYQKAIYGTQLSVGMRFGMMFETEESGKRRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MIMGSVEEKIKAGGLLSGAQSSILDEMKLLKELQDHSGSRKAIN)
SELWHACAGPLVCLPQVGSLSYYFPQGHSEQVAVSTKRTATSQIPNYPNLPSQLLCQV
QNVTLHADKETDEIYAQMSLKPVNSEKDVFPVPDFGLKPSKHPSEFFCKTLTASDTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WVVGDKVDAAASGKSEVYLSAVLQKPVRV"
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SNVAHELKLFLQHHQLPLGKDSRTGITEMVASVGHSCEKSADLLSQYMNYKVSGPCPD
DWSLAQKLILRGCEPLPRRRCFAKTLPKVGLNPFPISLWKPVSDKIVTWSGLGCKSFE
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/note="similar to putative DEAH helicase MFE16.9 in
Arabidopsis thaliana; likely non-functional due to two
frame-shifts and premature stop codons"
                                                                                                                                                                                                                                                                                                                                            41043.
                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana; non-functional due to a frame-shift"
                                                                                                                                                                                                                                                                                                                                                                                                             join(36926.
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|7499. .18764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/product="hypothetical transcription factor"
/protein ida"AAO14628.1"
/db_xref="GI:27450533"
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/protein_id="AAO14627.1
/db_xref="GI:27450532"
                                                                                                                                                                                note="likely the remains of a retroelement"
                                                                                                                                                                                                                                                                      note="likely the remains of a retroelement"
                                                                                                                                                                                                                                                                                                                                                                                   join(36926. .36970,36973. .37377)
/note="similar to hypothetical protein F6F9.11 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGLDVGGKPEKFEFVMFDIDRILRPGGLFWLDNFYCSNEEKKRDLTRLIERFGYKKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="similar to unknown protein K17E12.5 in Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="similar to IAA24/monopteros/ARF5 gene, F6F9.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MGSVSLKIGDGTARFKRATLCSSAVNLLMLFSVITTNLFALYAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
                                                                                     88.9%; Score 16; DB 8; Length 48843; 100.0%; Pred. No. 81;
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                       clone="XXFOS-802760E8"
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Homo sapiens chromosome UNK clone XXFOS-802760E8, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.

AC145678
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Chemistry: Dye-terminator Big Dye; 100% of 1
Assembly program: Phrap; version 0.99031
Consensus quality: 42380 bases at least Q30
Consensus quality: 44639 bases at least Q30
Consensus quality: 46559 bases at least Q30
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Direct Submission

Submitted (19-JUL-2003) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St.
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Sequencing vector: plasmid; 100%
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1 (bases 1 to 51797)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 51797)
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                       Location/Qualifiers
                                                                                                                                                                                                                      21234: contry cr. 21334: gap of unknown length 46167: contrig of 24833 bp in length
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49886: contig
                                                                                                              49986: gap of 
51797: contig
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47548: contig
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0: gap of unknown length
2: contig of 4172 bp in length
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                                                                                                                                    5 (bases 1 to 58068)
Waterston,R.H.
Direct Submission
Submitted (17-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                    Direct Submission
Submitted (11-MAR-2002) Genome
University School of Medicine,
MO 63108, USA
5 (bases 1 to 58068)
                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (03-FEB-2002) Genome
University School of Medicine,
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Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
             Direct Submission
Submitted (30-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63
On Mar 17, 2002 this sequence version replaced gi:19339131.
                                                                                                                                                                                                                                                                               Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                          The sequence of Homo sapiens Unpublished (2001)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                             Waterston, R.
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Center: Washington University Genome Sequencing Center
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46268. .47548
/note="assembly_name:Contig6"
/76/0 /0006
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3361. 7532
/note="assembly_name:Contig11"
7633. 12298
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49987. .51797
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Center project name: H_NH0267D02
                                 Center code: WUGSC
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MC. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

## SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org pBACe3.6

# NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-609N18, 2000 bp overlap; the clone sequenced to the right is CTD-2012I17, 2000 bp overlap. Actual end of this clone is at base position 105788 of CTD-2012I17.

Polymorphisms exist between AC093722 and AC109350.

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FEATURES
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5524. .5626
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3694. .3714
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1124. .1158
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6741. .7042
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2. .14853
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 AC092359 107129 bp DNA linear I Homo sapiens chromosome 5 clone RP11-341E24, WORKING
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Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 107044)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (26-FEB-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 26, 2002 this sequence version replaced gi:14589473.
Draft Sequence Produced by DOE Joint Genome Institute
WWW.jgi.doe.gov
                                                                                                                                                     ch 88.9%; Score 16; DB 9; 1 Similarity 100.0%; Pred. No. 74; 16; Conservative 0; Mismatches
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DOE Joint Genome Institute and Stanford Human Genome Center.
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20765. .21143
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22306. .22597
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21478. .22305
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tive 0; Mismatches
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les 16; Conserv
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Consensus quality: 105971 bases at least Q30
Consensus quality: 106638 bases at least Q30
Consensus quality: 106638 bases at least Q30
Estimated insert size: 181520; agarose-fp estimation
Batimated insert size: 18520; sum-of-contigs estimation
Quality coverage: 6.12 in Q20 bases; sum-of-contigs estimation
Quality coverage: 10.39 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. Gaps between the contigs
are are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.

This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

27925
28024: contig of 27924 bp in length
29250
29269: contig of 1245 bp in length
29270
29369: gap of unknown length
29270
107129: conteig of 77760 bp in length.
68444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (07-MAR-2002) Production Sequencing Facility, DOE Jo Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, On Mar 7, 2002 this sequence version replaced gi:14589548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (03-JUL-2001) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 3 (bases 1 to 107129)
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
Sequencing of Human Chromosome
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AC092359
AC092359.2 GI:19224822
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DOE Joint Genome Institute.
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CAAGCTTTTATAATAG
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sapiens (human)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
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/clone_lib="RPCI human
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Submitted (11-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 133244)
Swearengen-Shahid,S., Kozlowicz,A. and Dignan,G.
The sequence of Homo sapiens BAC clone RP11-23406
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens BAC clone RP11-23406 from AC104793 AC104793.4 GI:19909440
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Sulston, J.E. and Waterston, R.
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Submitted (03-APR-2002) Genome
University School of Medicine,
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Submitted (21-DEC-2001) Genome
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Genome Res. 8 (11), 1097-1108 (1998)
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Center project name: H_NH0234006
            Contact: sapiens@watson.wustl.edu
                                           Web site: http://genome.wustl.edu/gsc
                                                           Center: Washington University Genome Sequencing Center Center code: WUGSC
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dicine, 4444 Forest Park Parkway, St. Louis,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

FEATURES

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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP11-80B23, 2000 bp overlap.
Actual start of this clone is at base position 1 of RP11-234O6;
actual end is at base position 3275 of RP11-80B23.
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/mol_type="genomic DNA"
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

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Copyright (c) 1993 - 2005 Compugen
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US-09-949-016-15836
US-09-949-016-129476
US-09-949-016-129478
US-09-949-016-129478
US-09-949-016-129478
US-09-949-016-129559
US-09-949-016-129772
US-09-949-016-129843
US-09-949-016-129843
US-09-949-016-129843
US-09-949-016-129843
US-09-949-016-12664
US-09-949-016-15408
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Sequence 12, Appl
Sequence 8, Appli
Sequence 15836, A
Sequence 129375,
Sequence 129448,
Sequence 129488,
Sequence 129559,
Sequence 129559,
Sequence 129530,
Sequence 129701,
Sequence 129772,
Sequence 129772,
Sequence 129914,
Sequence 129914,
Sequence 129915,
Sequence 129916,
Sequence 154985,
Appli
Sequence 15663, A
Sequence 15664, A
Sequence 15409, A
Sequence 15410, A
Sequence 15411, A
Sequence 15411, A
Sequence 15413, A
Sequence 15413, A
Sequence 15413, A
Sequence 15413, A
Sequence 15414, A
Sequence 15414, A
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Query Match Best Local Matches 1	ORGAN FEATU NAME/ LOCAT OTHER OTHER 09-872	TITLE TITLE FILE R CURREN CURREN PRIOR	RESULT 1 US-09-872-051-12 US-09-872-051-12 ; Sequence 12, Applica ; Patent No. 6825400 ; GENERAL INFORMATION: ; APPLICANT: Monsantc ; APPLICANT: Hironak ; APPLICANT: Hironak ; APPLICANT: You, Ji ; APPLICANT: You, Ji	444 5	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
വാവാ	GANISM: Ar ATURE: AFTURE: CATION: (1) HER INFORM HER INFORM HER INFORM	OF INVENT REFERENCE: NAT APPLICAN NAT PLING NAT FILING APPLICATI APPLICATI FILING DA F	051-12 12, Applic 10. 6825400 INFORMATION INFORMATION ANT: Monsant ANT: Herona ANT: Herona ANT: You, J	114 144 144	115 115 114 114 114 114 114
nilarity Conser CCAAGCTT	ISM: Artificia RE: SOURCE KEY: SOURCE ION: (1)(18) INFORMATION: INFORMATION: -051-12	OF INVENTION OF INVENTION OF INVENTION OF THE PRESENCE: 38 IT APPLICATION FILING DATE: APPLICATION FILING DATE: APPLICATION FILING DATE: APPLICATION FILING DATE: APPLICATION OF SEQ ID OF	12 Application 825400 RMATION: Monsanto Co Behr, Carl Hironaka, Heck, Greg You, Jinson	77.8 77.8 77.8 77.8	83.3 83.3 83.3 83.3 83.3 77.8 83.3 77.8 77.8
100.0% imilarity 100.0% ; CONSETVATIVE ACCAAGCTTTTATAATAG                ACCAAGCTTTTATAATAG	icial Sequence e (18) ON: Agrobacter ON: er DN		2 Application US/0987205 25400 WATION: lonsanto Co Behr, Carl Hironaka, Catherine Heck, Gregory You, Jinsong	1328 1328 1332 1349	107925 107926 107926 107926 107926 687 687 822 999 1126 1328
0.0%; 0.0%; 0.TAG	acte	w HOHONGO YHO	;/09		
; Score 18; DB; Pred. No. 5.6; 0; Mismatches; 18; 18	l Sequence Agrobacterium tumefaciens er DN	nt PV-ZMGT32(nk603) B US/09/872,051 66-01 //213,567 //213,215 3 1/240,014 3	872051 ne	US-08-461-939B-58 US-08-464-000-58 US-09-489-039A-14 US-08-290-448A-73 ALIGNMENTS	US-09-949-016-11875 US-09-949-016-15406 US-09-949-016-15406 US-09-949-016-15406 US-09-949-016-15406 US-09-949-016-15407 US-09-621-976-9838 US-08-956-117E-608 US-08-956-117E-608 US-08-107-433-268 US-09-107-433-268 US-09-1134-001C-1178 US-09-124-001C-1178 US-09-124-001C-1178 US-09-477-251A-13 US-08-175-069A-58 US-08-175-069A-58
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RESULT 2
US-09-872-051-8
; Sequence 8, Application US/09872051
; Patent No. 6825400
; GENERAL INFORMATION:
; APPLICANT: MORSANTO CO
; APPLICANT: Behr, Carl

pron

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CURRENT APPLICATION NUMBER: US/09/872,051
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR FILING DATE: 2000-06-22
PRIOR REPLICATION NUMBER: 60/241,215
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/240,014
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 2000-10-13
VUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 1183
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LOCATION: (1) .. (1183)

OTHER INFORMATION: 1-164 Agrobacterium tumefaciens nos 3'
OTHER INFORMATION: 165-381 construct vector DNA
OTHER INFORMATION: 382-686 Zea maize plastid genes, rps11
OTHER INFORMATION: 687-1183 Zea maize genomic DNA
US-09-872-051-8
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                                                                                                                                                                       US-09-949-016-15836
                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Patent No. 6812339
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                   NUMBER OF
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Detec
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                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                           ORGANISM: Human
                                                                                                                                                                                                                                   LENGTH: 45587
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                                          ACCAAGCTTTTATAATA 17
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ACCAAGCTTTTATAATA 6014
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                                                                                  94.4%; Score 17; larity 100.0%; Pred. No. Conservative 0; Mismatch
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larity 100.0%;
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RESULT 4

RESULT 6 US-09-949-016-129417

Sequence 129417, Application US/09949016 Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

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                                                                                                                                                           ; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-129346
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US-09-949-016-129346
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows SEQ ID NO 129346
                                                                              Matches
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Best Local (
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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PRIOR FILING DATE: 2000-10-03
PRIOR PPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASCISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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15; Conservative
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CCAAGCTTTTATAAT 562
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                                                                              Conservative
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100.0%; Pred. No. 86;
tive 0; Mismatches
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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PATENT NO. 6812229.

PATENT INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANTION: POLYMORHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT TYMG DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 129417
LENGTH: 601
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 129488
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GENERAL INFORMATION:
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Best Local
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-09-949-016-129417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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100.0%; Pr
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100.0%; Pred. No.
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Pred. No.
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                                                                                            ASSOCIATED
OF DETECTION AND USES
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

PILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498
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                                                                                                                                                                                                                                                                                                       RESULT 10
US-09-949-016-129701
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US-09-949-016-129630
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                                                                                                                                                                                                                                                          Sequence 129701, Application US/09949016 Patent No. 6812339
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREEDER for Windows Version 4.0
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Best Local Similarity
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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TYPE: DNA
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100.0%; Pred. No. 86;
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RESULT 12
US-09-949-016-129843
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; ORGANISM: Human
US-09-949-016-129701
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US-09-949-016-129772
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Best Local Similarity
Matches 15; Conserv
SOFTWARE: FastSEQ for Windows Version SEQ ID NO 129843
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 129701
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              Sequence 129843,
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Best Local Similarity
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GENERAL INFORMATION:
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                                                     APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08.
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CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILLING DATE: 2000-10-20
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PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
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                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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100.0%; Pred. No.
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; ORGANISM: Human
US-09-949-016-129843
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US-09-949-016-129985
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                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 129985
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                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                   APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                         TYPE: DN
                                                                                                                                                   NUMBER OF SEQ ID NOS: 207012
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ORGANISM: Human
                                                    ORGANISM: Human
                                                                         DNA
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POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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RESULT 15

US-09-949-016-130056, Application US/09949016

Federat No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 130056

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-130056
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Search completed: February 10, 2005, 08:50:04 Job time : 6.53136 secs
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548 CCAAGCTTTTATAAT 562
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Maximum DB
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1: geneseqn1980s:*
2: geneseqn1990s:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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8 ABQ76678	10 ADC87620	12 ADK16049_4	8 ADA44289	8 ABZ73902	4 ABL20304	4 ABL10414	10 ADH61060	10 ADC42306	3 AAA48446	12 AD035611	10 ADC30185	12 ADK17054	6 ABK76160	4 AAH34926	6 ABV74652	11 ACN44736	6 ABL53728	6 ABK15245	6 ABK15249	B ID
Abq76678 Androgen	Adc87620 Human GPC	Continuation (5 of	Ada44289 Human sec	Abz73902 Secreted	Abl20304 Drosophil	Abl10414 Drosophil	Adh61060 Zebratish	Adc42306 cDNA enco	Aaa48446 Zebratish	Ado35611 Novel mou	Adc30185 Human nov	Adk17054 Nanoarcha	Abk76160 Bacillus	Aah34926 Human col	Abv74652 Human zin	Acn44736 Mouse gen	Abl53728 Human ERG	Abk15245 Corn nk60	Abk15249 Corn tran	Description

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ARTUS 294	AAV/4919	AAF1482/	ABX57529	ABT05259	ABS67082	ABS02355	AAI33833	AAC45230	AAC40800	AAC36726	ABS01738	AAI01706	ABS26774	AAK01737	AAK27192	ABA23236	3053	AAI33087	ABA53465	AAI11775	9826	6187	9T6/	110	5137
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### ALIGNMENTS

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RESULT 1
ABK15249
Probe; ss; rice actin 1 promoter; RA1; RA1 intron; chloroplast transit peptide gene; glyphosate resistance; corn; 5-enol-pyruvylshikimate-3-phosphate synthase; EPSPS; Hsp70 intron; transcriptional terminator; cauliflower mosaic virus 35S promoter; PV-ZMGT32; transgenic; nk603.
                                                                                                                                                                                           Agrobacterium tumefaciens. Oryza sativa.
                                                                                                                                                                                                                                                                 Corn transgene junction probe #4.
                                                                                                                                                                                                                                                                                 29-AUG-2003
08-MAY-2002
                                                                                                                                                                                                                                                                                                          ABK15249;
                                                                                                                                                                                                                                                                                                                          ABK15249 standard; DNA; 18 BP.
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                                                                                                                                                                                    Chimeric.
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(first ent
                                                                                                                                                                                                                                                                                   entry)
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22-JUN-2000; 2000US-0213567P. 13-OCT-2000; 2000US-0240014P. 13-OCT-2000; 2000US-0241215P. 02-JAN-2002. 15-JUN-2001; 2001EP-00202314. (MONS ) MONSANTO TECHNOLOGY LLC

Behr Œ, Hironaka C, Heck GR,

You J;

Novel DNA construct useful for producing a corn plant that tolerates application of glyphosate herbicide, comprises two transgene express cassettes. WPI; 2002-165871/22.

expression

Claim 8; Page 3; 25pp; English

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RESULT 2
ABK15245
ID ABK1
XX ABK1
XX ABK1
XX ABK1
XX Os;
DT 08-y
XX Csilc
XX Os;
XX Csilc
XX Seal
OS Escl
OS Escl
OS Chit
XX Syni
OS Chit
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                             22-JUN-2000;
13-OCT-2000;
13-OCT-2000;
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2000US-0240014P.
2000US-0241215P.
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/*tag= c

/note= "Corn page 187 . .1183

/*tag= d
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/note= "T-AGRTU.nos vector sequence"
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                                                                                                                                                                                                                                                                                                                                              "Corn genomic sequence"
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Pred. No.
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Best Local (
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                     A novel polypeptide-human ERG for coding this polypeptide.
                                                                                          Mao
                                                                                                                                                                     19-JUN-2000;
                                                                                                                                                                                                                                                                           haemopathy; HIV infe
anti-HIV; virucide;
                                                                                                                                                                                                                                                                                      ERG conjugated protein; human; leukaemia; lipoma; inflammation; haemopathy; HIV infection; cytostatic; antiinflammatory; haemos
                                                                                                                                                                                                                                                                                                                            Human ERG conjugated protein 72 PCR primer #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel DNA construct useful for producing a corn plant that tolerates application of glyphosate herbicide, comprises two transgene express
                                                                WPI; 2002-305400/35
                                                                                                                                            19-JUN-2000; 2000CN-00116558
                                                                                                                                                                                                02-JAN-2002.
                                                                                                                                                                                                                         CN1329029-A.
                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                         24-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                   ABL53728;
                                                                                                                                                                                                                                                                                                                                                                                                          ABL53728 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1183 BP; 295 A; 289 C; 280 G; 319 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vector sequences and corn sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MONS ) MONSANTO TECHNOLOGY LLC
                                                                                                                    (SHAN-)
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                                                                                          Xie
                                                                                                                    SHANGHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hironaka C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                      2000CN-00116558
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                                                                                                                  BIODOOR GENE DEV
                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
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therapy; PCR; primer; ss.
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Pred. No. 5.
                                   conjugated
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                                      72
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                                      and
                                    polynucleotide
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0

Example 5; Page 18 (Disclosure); 33pp; Chinese

XSSSSSSXXX

The present invention relates to novel human ERG conjugated pro (see ABB75713). The protein and its coding sequence are useful treatment of several diseases, such as medullary leukaemia, lip inflammation, immunological disease, haemopathy, development di and HIV infection. The present sequence is a PCR primer, which in an example from the invention

development disturbance primer, which was used

leukaemia, lipoma,

protein

72

E Or

RESULT 4 ACN44736/c

ACN44736 standard; DNA; 107320 BP

ACN44736;

18-NOV-2004

(first entry)

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N N

CCAAGCTTTTATAATA 17 CCAAGCTTTTATAATA 17

Query Match
Best Local Similarity
Matches 16; Conserv

Conservative

0

Mismatches

<u>,,</u>

Indels

0

Gaps

0

100.0%; 88.98;

Score 16; Pred. No.

DB 81;

6

Length 33;

Sequence 33

BP; 8 A; 6 C; 1 G; 18 T; 0 U; 0 Other;

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Best Loc
Matches
                           Query Match
                                                                                 The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (ii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (ii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma are a propensity to carcinoma; and (xi) for determining Carcinoma associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                  Recombinant nucleic acid useful for diagnosis comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002; 2002US-00087192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003; 2003WO-US006235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                        Sequence
                                                                                                                                                                                                                                                                                                        Claim
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Local Similarity
nes 16; Conserv
                                                                                                                                                                                                                                                                                                        SEQ ID NO 1333; Opp; English.
                                                         107320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carcinoma; lymphoma; cancer; murine;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence mCG2943.
                                                                                                                                                                                                                                                                                                                                                                                                                                         DISCOVERY
                                                         BP;
                                                        30076 A;
                           88.98;
               Score 16;
Pred. No.
                                                         19214 C;
   Mismatches
                                                           21901
                            DB 11;
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 <u>..</u>
                                                           35227 T;
                              Length 107320;
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U;
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 Gaps
                                                           Other;
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05-APR-2001

WO200122920-A2

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RESULT 5
ABV74652
ID ABV74652;
XX
AC ABV74652;
XY
AC ABV74652;
XX
TO 3-FEB-2003 (first XX)
DE Human zinc finger pr
XX
Human; zinc finger pr
XX
Homo sapiens.
XX
10-APR-2002.
XX
19-SEP-2000; 2000CN-
XX
19-SEP-2000; 2000CN-
XX
PR 19-SEP-2000; 2000CN-
XX
PR 19-SEP-2000; 2000CN-
XX
PR 19-SEP-2000; 2000CN-
XX
PR (BODE-) BODE GENE DE
XX
PI Mao Y, Xie Y;
XX
PI Mao Y, Xie Y;
XX
PI Mao Y, Xie Y;
XX
PI Mao Y, The present inventic CC ABB98772). The zinc CC treating cancer and CC which was used in au
XX
Sequence 33 BP; 6 A
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RESULT 6
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Matches
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                                                                     Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 17; ss.
                                                                                                                                                                                                                                                                                                                                                                         ABB98772). The zinc finger protein treating cancer and HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-548869/59
                                               Homo
                                                                                                        Human colon cancer antigen
                                                                                                                                03-SEP-2001
                                                                                                                                                        AAH34926;
                                                                                                                                                                              AAH34926 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                 which was used in an example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     finger protein 64.90 PCR primer #4
                                                                                                                                                                                                                                                                                                                                                                                                                           Page 18 (Disclosure); 34pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             finger protein 64.90; cancer; HIV infection; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to Human
                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                    83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.
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                                                                                                                                                                                                                                                                                                                                                                       protein and its coding sequence fection. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                         encoding cDNA SEQ ID NO:2008
                                                                                                                                                                                                                                                                                           <u>.</u>
                                                                                                                                                                                                                                                                                                      Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                 from the
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                                                                                                                                                                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                               its coding sequence is present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                      zinc finger protein
                                                                                                                                                                                                                                                                                                                                         U; 0 Other;
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a PCR primer,
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are useful
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for

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AC ABK761
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DT 13-AUG
DE Bacill
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Differ
KW Differ
KW Differ
KW physio
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Bacill
XX
DS Bacill
XX
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and vacchine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The co-cancer antigens have cytostatic activity and can be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding useful for preventing,
                              06-OCT-2000; 2000US-00680598
27-MAR-2001; 2001US-0279526P
                                                                                                                                                                                                                                                                                                                                                                            Differential gene expression; genomic sequenced tag; GST altered culture condition; environmental stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus licheniformis genomic sequence tag
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                                                                                                                                                                             11-APR-2002.
                                                                                                                                                                                                                                   WO200229113-A2
                                                                                                                                                                                                                                                                                             Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                    physiological
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468
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                                                                                                                                                                                                                                                                                                                                                    provocation;
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tive 0; Mismatcl

y 4277 human of
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and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T; 0 U; 8 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (N) and proteins (P), where the cancer antigens. The colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GST) #3451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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RESULT 8
ADK17054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, environmental stress or other physiological provocation. Extensive follow up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence (GST) used in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring global expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NOVO)
                                                                                                       01-MAY-2003; 2003WO-US013699
                                                                                                                                                                                                                 Nanoarchaeum equitans
                                                                                                                                                                                                                                                                       cancer-associated gene; CA gene; cancer; carcinoma; lymphoma; leukaemia;
                                                                                                                                                                                                                                                                                                         Nanoarchaeum equitans cancer-associated (CA) gene #503
                                                                                                                                                                                                                                                                                                                                             06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                     ADK17054 standard; DNA; 786 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a method of monitoring differential expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
                                                                     01-MAY-2002; 2002US-0377447P
                                                                                                                                             13-NOV-2003
                                                                                                                                                                               WO2003093434-A2
                                                                                                                                                                                                                                                    ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-416684/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berka
                                 (DIVE-) DIVERSA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CCAAGCTTTTATAAT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOVOZYMES BIOTECH INC. NOVOZYMES AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAAGCTTTTATAAT 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 3451; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clausen IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 145 A; 151 C; 118 G; 135 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                               (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.3%; but
100.0%; Prr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15;
Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Stetter KO,

Waters E,

Kretz K,

Podar M,

Richardson

Η,

Claim 5; SEQ ID NO 1006; 251pp; English.

New recombinant cancer-associated genes, such as KCNJ9, diagnosing or treating carcinoma, e.g. breast, colon, r cervical, or skin cancers, lymphomas, or leukemia.

colon, rectal, pancreatic

useful

for

WPI; 2004-053041/05. P-PSDB; ADK17055.

Noordewier

The invention comprises then amino acid and coding sequences of cancer-associated (CA) genes isolated from Nanoarchaeum equitans. The invention also comprises the Nanoarchaeum equitans genome. The DNA and protein sequences of the invention are useful for diagnosing and treating cancer (e.g. carcinoma, lymphoma, or leukaemia). The present DNA sequence represents a Nanoarchaeum equitans CA gene of the invention.

Sequence 786 BP;

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ADC30185/c
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Best Local S
Matches 15
                                                                                                                      Tang
Zhou
                                                                                                                                                                                                                                                                                                 Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antillcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
                             New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platel disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                         WPI; 2003-371981/35.
P-PSDB; ADC31156.
                                                                                                                                                                                                                                                                                                                                                                                           Human novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADC30185 standard; cDNA; 1137
                                                                                                                                                                                                  24-SEP-2002; 2002WO-US030474.
                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                            Haley-Vicente
                                                                                                                                                                                                                         10-APR-2003
                                                                                                                                                                                                                                              WO2003029271-A2
                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                              , Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAGCTTTTATAATA
                                                                                                                       Zhang J,
Ghosh M,
                                                                                                                                                                                                                                                                                                                                                                                          cDNA sequence, SEQ ID NO:267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                              2001US-0324631P
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                           'n
                                                                                                                      3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 A; 112 C; 135 G; 244 T; 0 U; 0 Other;
                                                                                                          J, Ren F,
Wang D,
Drmanac R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.3%; Score 15;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
                                                                                                            RT;
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                                                                                                                                 Xue
                                                                                                                       ма Y,
                                                                                                                       AJ, Zhao QA,
Y, Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.9e+02;
hes 0;
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                                                                                                                       Wang
                                                                                                                       Wang J,
Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 786;
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                                                                                                                      Weng G;
                                                                                                                                 Wehrman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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CC ADC3089) and the polypeptides they encode (ADC3089-ADC31860). The CC ADC3089) and the polypeptides they encode (ADC30890-ADC31860). The CC invention also relates to nucleic acid sequences over 99% identical with CC the novel human cDNAs. The invention additionally encompasses expression CC vectors and host cells comprising a nucleic acid of the invention; the CC against a polypeptide of the invention; an antibody CC against a polypeptide of the invention, and methods of CC invention further discloses methods to a polypeptide of the invention. The CC invention further discloses methods to a polypeptide of the invention. The CC invention further discloses methods of polypeptide of the invention. The CC invention methods for the identification of compounds that modulate the CC expression or activity of the polypucleotide and/or polypeptide; and 767 CC contig sequences corresponding to the cDNA sequences of the invention CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628 (ADC3394). The nucleic acids and polypeptides of the invention are identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of date and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's CC disease and other neurodegenerative diseases, anaemia, platelet concer. The nucleic acids may also be used as hybridisation probes or primers, and in processing antibodies, as molecular weight markers, are also useful in generating antibodies, as molecular weight markers, are also as polypeptides. The present sequence represents a specifically
                                                                                                                                        and as food supplements. The present sequence represents a specifically claimed human cDNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                             Sequence 1137 BP; 295 A; 260 C; 292 G; 290 T; 0 U; 0 Other;
                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
   DB 10;
Length 1137;
                                                                                                                                                                                                           data for
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Ś
                      Matches
                              Query Match
Best Local
      -
                        15;
                              Similarity
ACCAAGCTTTTATAA 15
                       Conservative
                              83.3%; Score 15; 100.0%; Pred. No.
                        ٥.
                        Mismatches
                                 1.8e+02;
                        .
;
                         Indels
                        0
                         Gaps
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0

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ADO35611/c
ID ADO35611 standard; DNA; 1248
                                                   RESULT 10
AD035611;
                            ВÞ
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398

ACCAAGCTTTTATAA 384

Mus mouse; murine; cancer; psoriasis; ulcerative colitis; inflammation; ischaemic heart disease; thrombosis; immune disorder; bacterial disorder; WO2004046310-A2 disorder; ds; gene.

Novel mouse 26-AUG-2004

gene

sequence #284.

(first entry)

03-JUN-2004.

24-OCT-2003;

2003WO-US033948.

15-NOV-2002; ; 2002US-0426916P. ; 2002US-0431158P. ; 2002US-043145P. ; 2002US-0431606P. ; 2003US-0476621P. ; 2003US-0476632P.

04-DEC-2002; 05-DEC-2002; 05-DEC-2002; 09-JUN-2003; 09-JUN-2003;

Claim 1; SEQ ID NO 267; 1185pp; English

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RESULT 11
AAA48446/c
ID AAA484
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Best Local S
Matches 15
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08-JUL-2003;
08-AUG-2003;
08-AUG-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises 744 novel mouse DNA sequences (genes). The DN sequences of the invention are useful for treating cancer, psoriasis, ulcerative colitis, inflammation, ischaemic heart disease, thrombosis immune disorders, bacterial disorders and viral disorders. The preser nucleic acid represents a mouse DNA sequence of the invention. NOTE: present DNA sequence is not shown in the specification, but has been retrieved from the WIPO website.
                                                                                                                                                                                CDS
                                                                                                                                                                                                                                         Zebrafish; parathyroid hormone type-3 developmental disorder; physiological
                                                                                                                                                                                                                                                                                          15-SEP-2003
27-OCT-2000
                                                                                                                                                                                                                                                                                                                                           AAA48446 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mouse nucleic acid molecules and polypeptides, useful cancer, psoriasis, ulcerative colitis, inflammation, isch
P-PSDB; AAY99601
                             Jueppner H,
                                                (JUEP/)
(RUBI/)
                                                                               30-NOV-1998;
                                                                                                  30-NOV-1999;
                                                                                                                      08-JUN-2000.
                                                                                                                                         WO200032775-A1
                                                                                                                                                                                                              Danio
                                                                                                                                                                                                                                                                       Zebrafish
                                                                                                                                                                                                                                                                                                                        AAA48446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FIVE-) FIVE
          2000-412323/35.
                                                                                                                                                                                                                                                                                                                                                                                            931
                                                                                                                                                                                                              rerio.
                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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                                                JUEPPNER H. RUBIN D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             psoriasis, ulcerative or thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1248 BP; 452 A; 245 C; 236 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Į,
                                                                                                                                                                                                                                                                                                                                                                                           CCAAGCTTTTATAAT
                                                                                                                                                                                                                                                                                                                                                                                                             CCAAGCTTTTATAAT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 284; 263pp; English
                                                                                                                                                                                                                                                                       parathyroid hormone type-3 receptor PTH3R coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2003US-0485217P.
2003US-0485359P.
2003US-0493332P.
2003US-0493336P.
                             Rubin DA
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIME THERAPEUTICS
                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chu
                                                                               98US-0110467P
                                                                                                  99WO-US028207.
                                                                                                                                                                     Location/Qualifiers
394. .2022
/*tag= a
                                                                                                                                                             /product= "PTH3R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee
                                                                                                                                                                                                                                                                                                                                                                                            917
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                            ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INC
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                          receptor; disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8e+02
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                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                          PTH3R;
neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       iseful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kamiya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    psoriasis,
thrombosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: The
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 12
ADC42306/c
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Matches
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ADC42306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the parathyroid hormone type-3 receptor (PTH3R) coding sequence from the zebrafish. It was obtained by sequencing a cDNA clone. The gene and protein can be used to detect diseases in man where the receptor is either overexpressed or underexpressed, and they can be used to treat these diseases, which may be developmental, physiological or neurological disorders. They can also be used to identify agonists and antagonists which can be used in a similar manner. In addition, the gene can be used for chromosome identification. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                            WPI;
                                                                                                                                                                              30-NOV-1998;
                                                                                                                                                                                                                          01-APR-2003.
                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                    parathyroid
parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acids encoding parathyroid hormone receptors PTH1R useful for treating diseases or disorders associated with impaireceptor functions comprises a specific nucleotide sequence.
                                                               Novel nucleic acid comprising a polynucleotide encoding parathyroid hormone/parathyroid hormone-related peptide receptor, useful for
                                                                                                 P-PSDB;
                                                                                                                                  Jueppner H,
                                                                                                                                                                                                    30-NOV-1999;
                                                                                                                                                                                                                                                US6541220-B1.
                                                                                                                                                                                                                                                                                                                                      Danio rerio.
                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC42306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                           PTH1R;
                                                                                                                                                         (GEHO)
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                                                                                                             2003-754511/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   μ
                                                                                                                                                                                                                                                                                                                                                          gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                         GEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                  ADC42307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCAAGCTTTATAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCAAGCTTTTATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 1D; 111pp;
                                                      identification.
                                                                                                                                                        HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                 hormone; PTH; PTH-related peptide; PfHrP;
                                                                                                                                                                                                                                                                                                                                                                      hormone receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                      zebrafish parathyroid hormone receptor PTH3R seq
                                                                                                                                                                               98US-0110467P
                                                                                                                                                                                                    99US-00449632
                                                                                                                                                                                                                                                                                                    394. .2022
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                     /product= "Zebrafish PTH3R"
/note= "Parathyroid hormone
                                                                                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zebrafish PTH3R cDNA
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The present invention relates to novel parathyroid hormone (PTH) and parathyroid hormone related protein (PTHYP) receptors PTHIR and PTHJR isolated from zebrafish. The invention is useful in the diagnosis and prognosis of certain diseases and disorders that express significantly decreased levels of PTHIR and PTHJR. The invention is also useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-AUG-2003
                                                                                                                                                             Claim
                                                                                                                                                                                                             receptor-related diseases.
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                                                                                                                                                                                                                                      parathyroid hormone receptors designated PTH1R and PTH3R isolated \mathfrak m zebrafish are useful to diagnose and treat parathyroid hormone
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DB; ADH61061.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster expressed polynucleotide SEQ ID NO 25724.
                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16175) and the encoded proteins (ABB57737, sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
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                                                                                                      discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-BB72072). The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 25724; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                New isolated nucleic acid
genes from Drosophila and
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P-PSDB; ABB66311.
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11-JUL-2000;
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Best Local :
                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                           Sequence 8897 BP; 2656 A; 1738 C; 1855 G; 2648 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid genes from Drosophila and
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 12385; 21pp + Sequence Listing; English.
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                                                           83.3%; Score 15; DB 4; Length 8897; 100.0%; Pred. No. 1.5e+02; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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Search completed: February 10, 2005, 13:44:15 Job time: 22.6055 secs

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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

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Copyright (c) 1993 - 2005 Compugen Ltd.
/ Cgm2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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/ Cgm2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	% Query Match Length DB ID	Length	89	ID	Description
1	18	100.0	18	و و	US-09-872-051-12	Sequence 12, App
N	18	100.0	18	18	US-10-790-430-12	Sequence 12, Appl
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4	18	100.0	1183	18	US-10-790-430-8	Sequence 8, App
ი 5	16	88.9	612	18	US-10-425-115-76005	Sequence 76005, A
ი 6	16	88.9	107320	13	US-10-087-192-1333	Sequence 1333, Ap
c 7	15	83.3	440	17	US-10-424-599-142571	Sequence 142571,
80	15	83.3	468	15	US-10-106-698-2018	Sequence 2018, Ap
9	15	83.3	533	13	US-10-027-632-194059	Sequence 194059,
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Sequence 43, Appl Sequence 881, App Sequence 213307, Sequence 213308,	39839, 39839, 39839, 77058, 77058,	e 10849, e 10846, e 18546, e 17038,	147,	1368 1369 691 2477 2500	Sequence 194858, Sequence 194859, Sequence 194859, Sequence 31469, A Sequence 31469, A Sequence 3, Appli Sequence 254, App Sequence 6944, App Sequence 10. Appli

#### ALIGNMENTS

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TYPE: DNA ORGANISM: FEATURE: NAME/KEY: LOCATION: OTHER INF OTHER INF	PRIOR I PRIOR I PRIOR I PRIOR I PRIOR I PRIOR I PRIOR I PRIOR I	APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF II TITLE OF II FILE REFER CURRENT AP CURRENT FI PRIOR APPL	1 872- ence nt 1 RAL
TYPE: DA ORGANIAN: Artificial Seq FEATURE: NAME/KEY: SOUTCE LOCATION: (1)(18) OTHER INFORMATION: Agrob OTHER INFORMATION: ET DN US-09-872-051-12	PRIOR PELLIANG DATE: 2000-00-22 PRIOR APPLICATION NUMBER: 60/ PRIOR FILING DATE: 2000-10-13 PRIOR APPLICATION NUMBER: 60/ PRIOR FILING DATE: 2000-10-13 PRIOR FILING DATE: 2000-10-13 NUMBER OF SEQ ID NOS: 16 SOFTWARE: PatentIn version 3. SOFTWARE: PatentIn version 3. LENGTH-18	APPLICANT: Behr, Carl APPLICANT: Hironaka, Catheri APPLICANT: Heck, Gregory APPLICANT: You, Jinsong TITLE OF INVENTION: Corn Even TITLE OF INVENTION: Thereof FILE REFERENCE: 38-21 (52259) CURRENT APPLICATION NUMBER: 00 CURRENT FILING DATE: 2001-06 BRIOR APPLICATION NUMBER: 607	RESULT 1  US-09-872-051-12  US-09-872-051-12  ; Sequence 12, Application U ; Patent No. US20020013960A1 ; GENERAL INFORMATION: ; APPLICANT: Monsanto Co
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TYPE: DNA ORGANISM: Artificial Sequence FEATURE: FEATURE: NAME/KEY: source LOCATION: (1)(18) OTHER INFORMATION: Agrobacter OTHER INFORMATION: er DN 19-872-051-12	PRIOR PILLING DATE: 2000-00-22. PRIOR APPLICATION UNMBER: 60/2 PRIOR FILING DATE: 2000-10-13 PRIOR APPLICATION NUMBER: 60/2 PRIOR FILING DATE: 2000-10-13 NUMBER OF SEQ ID NOS: 16 SOFTWARE: PatentIn version 3.0 SOFTWARE: PatentIn version 3.0 LENGTH-18	APPLICANT: Behr, Carl APPLICANT: Hironaka, Catherine APPLICANT: Heck, Gregory APPLICANT: You, Jinsong TITLE OF INVENTION: Corn Event P TITLE OF INVENTION: Thereof FILE REFERENCE: 38-21 (52258) B CURRENT APPLICATION NUMBER: US/0: CURRENT FILING DATE: 2001-06-01 BRIOR APPLICATION NUMBER: 60/213	/098
TYPE: DNA ORGANISM: Artificial Sequence FEATURE: NAME/KEY: source LOCATION: (1)(18) OTHER INFORMATION: Agrobacterium tumefaciens nos 3' terminator and rice actin promother information: er DN OTHER 1NFORMATION: er DN	PRIOR APPLICATION NUMBER: 60/241,215 PRIOR APPLICATION NUMBER: 60/240,014 PRIOR FILING DATE: 2000-10-13 PRIOR FILING DATE: 2000-10-13 PRIOR FILING DATE: 2000-10-13 NUMBER OF SEQ ID NOS: 16 SOFTWARE: PatentIn version 3.0 SQ ID NO 12 FRIORTH: 18	APPLICANT: Behr, Carl APPLICANT: Hironaka, Catherine APPLICANT: Heck, Gregory APPLICANT: You, Jinsong TITLE OF INVENTION: Corn Event PV-ZMGT32( TITLE OF INVENTION: Thereof FILE REFERENCE: 38-21(52258)B CURRENT FILING DATE: 2001-06-01 CURRENT FILING DATE: 2001-06-01 FRIOR APPLICATION NUMBER: 60/213,567 PRIOR APPLICATION NUMBER: 60/213,567	SULT 1 :09-872-051-12 Sequence 12, Application US/09872051 Patent No. US20020013960A1 GENERAL INFORMATION: APPLICANT: Monsanto Co
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; APPLICANT: Heck, Gregory
APPLICANT: You, Jinsong
; TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) an;
TITLE OF INVENTION: Thereof
; FILE REFERENCE: 38-21(52258)B
; CURRENT APPLICATION NUMBER: US/09/872,051
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/213,567
; PRIOR APPLICATION NUMBER: 60/241,215
; PRIOR APPLICATION NUMBER: 60/241,215
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Patent No. US20020013960A1
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CURRENT FILING DATE: 2004-03-01
PRIOR APPLICATION NUMBER: US/09/872,051
PRIOR FILING DATE: 2001-06-01
                                                                                                                                                                                         APPLICANT: Monsanto Co
APPLICANT: Behr, Carl
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PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR FILING DATE: 2000-10-13
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APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Detec
TITLE OF INVENTION: Thereof
                                                                                                                                                         APPLICANT:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/240,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/790,430
CURRENT FILING DATE: 2004-03-01
PRIOR APPLICATION NUMBER: US/09/872,051
PRIOR FILING DATE: 2001-06-01
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PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 38-21 (52258) B
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LOCATION: (1)..(1183)
OTHER INFORMATION: 1-164 Agrobacterium tumefaciens 1
OTHER INFORMATION: 165-381 construct vector DNA
OTHER INFORMATION: 382-686 Zea maize plastid genes,
OTHER INFORMATION: 687-1183 Zea maize genomic DNA
                                                                                                                                                    LOCATION: (1)..(1183)
OTHER INFORMATION: 1-164 Agrobacterium tumefaciens r
OTHER INFORMATION: 165-381 construct vector DNA
OTHER INFORMATION: 382-686 Zea maize plastid genes,
OTHER INFORMATION: 687-1183 Zea maize genomic DNA
                                                                                                                                                                                                                                          FEATURE: NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                               ENGTH:
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                                                                                    Similarity
                                ACCAAGCTTTTATAATAG 18
                                                                                                                                                                                                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heck, Gregory
You, Jinsong
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                                                                    Conservative
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Pred. No.
                                                                                    Score 18; DB 18; Pred. No. 4.5;
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US-10-425-115-76005/c
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US-10-087-192-1333/c
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RESULT 7
US-10-424-599-142571/c
; Sequence 142571, Application US/10424599
; Publication No. US20040031072A1
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; NAME/KEY: misc feature
; LOCATION: (1).T.(107320)
; OTHER INFORMATION: n = A,T,C or
US-10-087-192-1333
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
FULE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 76005
LENGTH: 612
TYPE: NA
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Publication No. US20040214272A1
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APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric
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Publication No. US20020182586A1
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SEQ ID NO 1333
LENGTH: 107320
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                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER FILE REFERENCE: 529452000122 CURRENT APPLICATION NUMBER: US/10/087,192 CURRENT FILING DATE: 2002-03-01 PRIOR APPLICATION NUMBER: US 09/747,377 PRIOR FILING DATE: 2001-03-02 PRIOR FILING DATE: 2001-03-02 PRIOR FILING DATE: 2001-03-02
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16; Conserv
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                                                                                                                  CCAAGCTTTTATAATA 79972
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Conservative
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Pred. No.
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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_99757C.1
US-10-424-599-142571
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US-10-106-698-2018
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                                                                                                                      RESULT 9
US-10-027-632-194059
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CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR APPLICATION NUMBER: DCT/US00/26524
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-01-03
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
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SEQ ID NO 142571
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                                                                              Sequence 194059, Application US/10027632
Publication No. US20020198371A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2018
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Best Local Similarity
                                                           GENERAL INFORMATION:
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APPLICANT: Cao Yongwei
TITLE OP INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OP INVENTION: Plants and Uses Thereof for Plant Improvement
PILE REFERENCE: 38-21(5323)8
CURRENT PRICTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                      Matches
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APPLICANT: Kovalic David
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APPLICANT: Wang, David G. TITLE OF INVENTION: Ident TITLE OF INVENTION: Poly
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ORGANISM: Glycine max
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LOCATION: (434)...(434)
OTHER INFORMATION: n equals a,t,g, or
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Local Similarity 100.0%;
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Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
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Pred. No.
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Pred. No.
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hes 0;
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT EILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12

FILE REFERENCE: 108827.129

PRIOR APPLICATION NUMBER: US 60/198,676

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Best Local S
Matches 15
                                   Matches
                                                       Best
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Publication No. US20030204075A9
GENERAL INFORMATION:
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-10-027-632-194059
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
                                                                                                              ORGANISM: Human
10-027-632-194059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                 PRIOR FILING DATE:
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PRIOR APPLICATION NUMBER: US 60/185,218
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                                                                                                                                                    TYPE: DNA
                                                                                                                                                                      LENGTH:
                                                       Local
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APPLICATION NUMBER: US 60/193,483
FILING DATE: 2000-03-29
APPLICATION NUMBER: US 60/185,218
FILING DATE: 2000-02-24
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FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
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APPLICATION NUMBER: US 60/156,358
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2 CCAAGCTTTTATAAT 16
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                                     Conservative
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100.0%; Pred. No. 1.
tive 0; Mismatches
                                 83.3%; Score 15;
100.0%; Pred. No.
tive 0; Mismatch
                                     Mismatches
                                                                         DB 17;
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                                                   1.7e+02;
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                                                                       Length 533;
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; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: (1)...(613)
; OTHER INFORMATION: n = A,T,C
US-10-027-632-194858
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; Sequence 194858, Application US/10027632
; Publication No. US20020198371A1
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                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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Best Local S
Matches 15
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PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR EILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version
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TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085,500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                          PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Bacillus licheniformis
                                                                                                                  TYPE: DNA
ORGANISM: Human
                                                                                                                                                               ENGTH: 613
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nes 15; Conserv
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                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/146,002
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o. US20020146721A1
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US-10-027-632-194858/c
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Best Local
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Publication No. US20030204075A9
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Best Local
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PRIOR EILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
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NOTE: PastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
FILE REFERENCE: 108827.129
                                                  CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR FILING DATE: 2000-04-20 PRIOR FILING DATE: 2000-04-20
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PRIOR APPLICATION NUMBER: US 60/167,363
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                                                                                                                                                                        APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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                PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR FILING DATE: 2000-03-29
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ORGANISM: Human
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LOCATION: (1)...(613)
OTHER INFORMATION: n = A,T,C
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APPLICATION NUMBER: US 60/185,218
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15; Conservative
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100.0%; Pred. No.
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CAAGCTTTTATAATA 128

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; LOCATION: (1)...(613)

; OTHER INFORMATION: n = A,T,C

US-10-027-632-194859
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US-10-027-632-194859/c
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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LENGTH: 613
                                                          Query Match
Best Local 9
                                           Matches
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ORGANISM: Human
FEATURE:
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PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US
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PRIOR
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
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LOCATION: (1)...(613)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                            ORGANISM: Human
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FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
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                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/156,358 FILING DATE: 1999-09-28 APPLICATION NUMBER: US 60/146,002
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CAAGCTTTTATAATA 17
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100.0%; Pr
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ALIGNMENTS

#### RESULT 1 CE238229/c LOCUS DEFINITION REFERENCE AUTHORS VERSION KEYWORDS S SOURCE COMMENT ACCESSION FEATURES Query Match Best Local S Matches 17 TITLE JOURNAL MEDLINE ORGANISM PUBMED source 651 bp DNA linear GSS 25-SEP-2003 tigr-gss-dog-17000333406145 Dog Library Canis familiaris genomic, genomic survey sequence. CE238229 CE238229 CE238229.1 GI:35393987 GSS. 17; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. 1 (bases 1 to 651) Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C. 2 CCAAGCTTTTATAATAG 18 Canis familiaris (dog) Canis familiaris Contact: Kirkness EF The Institute for Genomic Research Department of Eukaryotic Genomics, Rockville, MD 20850, USA Tel: 301-838-0200 Fax: 301-838-0208 The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003) Class: shotgun 14512627 Email: ekirknes@tigr.org Similarity Conservative /clone lib="Dog Library" /note="Site 1: BstXI; Lik peripheral blood" /organism="Canis familiaris" /mol type="genomic DNA" /strain="Standard Poodle" /db_xref="taxon:9615" ocation/Qualifiers . 651 94.4%; Score 17; 100.0%; Pred. No. 0; Mismatches Libraries were prepared from DB 29; TIGR, 9; <u>;</u> Length 651; 9712 Medical Center Drive Indels ٥, Gaps 0;

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Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished (2002)
Contact: Nori Satoh
Department of Zoology
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
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Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
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BP008680 Nori Satoh unpublished cDNA library, young adult Ciona
intestinalis cDNA clone ciad49h02 5', mRNA sequence.
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                                                                                                                        Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502,
Tel: 81-75-753-4081
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BW295435 Nori Satoh unpublished cDNA library, neural intestinalis cDNA clone cinc010pl3 5', mRNA sequence
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Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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Department of Zoology
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                                                                                     satoh@ascidian.zool.kyoto-u.ac.jp.
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/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished
adult"
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
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/mol type="mRNA"
/db xref="raxon:7719"
/clone="ciad49h02"
                                                                   Location/Qualifiers
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100.0%; Pred. No. 99;
tive 0; Mismatches
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                                                                                                                                                                                                                                               54
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Contact: Nori Satoh
Department of Zoology
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AV906194 Nori Satoh unpublished cDNA library, young adult Ciona
intestinalis cDNA clone rciad65c15 3', mRNA sequence.
AV906194
                                                                                                                            ZMMBBc0564122r ZMMBBc Zea genomic survey sequence. CL225702
                                                                                                                                                                                                                                                                          1 ACCAAGCTTTTATAAT 16
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Sakyo-ku, Kyoto, Kyoto
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                  GSS.
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Location/Qualifiers
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1 (bases 1 to 199)
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/dev stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young adult"
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/mol_type="mRNA"
/db_xref="taxon:7719"
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tive 0; Mismatches
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Query Match 88.9%; S
Best Local Similarity 100.0%;
Matches 16; Conservative 0;
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Tel: 732 445 3801
Fax: 732 445 5735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV906393 Nori Satoh unpublished cDNA library, young adult Ciona intestinalis cDNA clone rciad65n15 3', mRNA sequence.
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Class: BAC ends
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Kohara, Y. and Shin-i, T. Expressed genes in Ciona intestinalis
Unpublished (2000)
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                                                                                                                                                                                                                                                               Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                Contact: Nori Satoh
Department of Zoology
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                                                                                /tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished adult"
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/mol_type="genomic DNA"
/cultivar="B73"
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/note="Vector: pTARBAC1.3; Site_1:
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/clone_lib="ZMMBBc"
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/clone="rciad65n15"
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1 (bases 1 to 357)

Mahairas, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S., Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E. Construction of a Characterized Clone Resource for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mahairas GG, Zackrone University of Washington Seattle, WA 98195, USA Tel: (206) 616-8744 Fax: (206) 685-7301
                                                                                                                                                                                                                                                                                                                                       w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: kzackron@u.washington.edu
Sequence Tagged Connector
Plate: CT 772 row: H column: 1
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Unpublished (1997)
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                                                                                                                                                                                    AV891743 Nori Satoh unpublished cDNA library, young aintestinalis cDNA clone rciad26f24 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                        16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B39844.1 GI:2544096
 Satoh,N., Satou,Y., Kohara,Y. and Snil
Expressed genes in Ciona intestinalis
Unpublished (2000)
                                                 Eukaryota; Metazoa; Chordata; Urochordata; Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 363)
                                                                                                 Ciona intestinalis
Ciona intestinalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: BAC ends
                                                                                                                                                      AV891743.1 GI:16880769
                                                                                                                                                                      AV891743
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop: 357.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="CIT Human Genomic Sperm Library (/note="Organ: sperm; Vector: pBeloBAC11; BAC E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=CT 772 Col=15 Row=H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'sex="M"
                                                                                                                                                                                                                                                                                                                                                                   88.9%; >>\
100.0%; Pr
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                                                                                                                                                                                                                                                                                                        153
                                                                                                                                                                                                                                                                                                                                                                        ; Score 16; DB
%; Pred. No. 1e+
0; Mismatches
                                       Kohara, Y. and Shin-i, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 bp DNA linear GSS 18-OCT-
CIT Human Genomic Sperm Library C Homo
Plate=CT 772 Col=15 Row=H, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              column: 15
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                                                                                                                                                                                                                                                                                                                                                                                                          DB 8;
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 357;
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Clones

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adult

Enterogona;

EST 09-NOV-2001 adult Ciona

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Genomic 20,000 Sequence

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SOURCE
ORGANISM
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VERSION
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B55409
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Best Local Similarity
Matches 16; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 382)
Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya Simon,M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
                                                                                                                                                                                                                                                                                                                             Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                              Class: BAC ends.
                                                                                                                                                                                                                                    end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                      Clones are available from
                                                                                                                                                                                                                                                                                  Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                       Use of a random BAC End Sequence Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Nori Satoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCAAGCTTTTATAAT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCAAGCTTTTATAAT 16
                                                                                                                                                                                                                            primer: M13-21
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301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:5379336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:2609743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
                                     /cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="whole animal"
/dev_stage="young adult"
/dlone_lib="Nori Satoh unpublished cDNA library, young
                                                                                                                                                                                           ocation/Qualifiers
                                                                                       sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="rciad26f24"
                                                                                                       clone="387A19"
                                                                                                                     db_xref="taxon:9606"
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B98924
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VERSION
KEYWORDS
SOURCE
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B45104
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DEFINITION
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DEFINITION
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                                                                                                                                 B98924 432 bp
CIT-HSP-2174P18.TF CIT-HSP Homo
                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mahairas GG, Zackrone KD,
University of Washington
Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CAAGCTTTTATAATAG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Tagged Connector Plate: CT 782 row: L cc Class: BAC ends
                                          Homo sapiens
                                                                                         B98924.1
                                                                                                        B98924
                                                                                                                     genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: kzackron@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tagged Connectors
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                                                         Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 431.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (206) 616-8744
(206) 685-7301
                                                                                                                                                                                                                                                                                      Conservative
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                                                                                         GI:3026734
                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                         clone="Plate=CT 782 Col=5
                                                                                                                                                                                                                                                                                                                                                                                                           sex="M"
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100.0%; Pr
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B45104 431 bp DNA linear GSS
HS-1060-B1-F03-MR.abi CIT Human Genomic Sperm Library C
sapiens genomic clone Plate=CT 782 Col=5 Row=L, genomic
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 432)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="CIT Human Genomic Sperm Library C" /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                    sapiens
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                                                                                                                                                                                                                                 genomic
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ACCESSION
VERSION
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Matches 16; Conser
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Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
Unpublished (1998)
Unpublished (1998)
Other GSSs: CII-HSP-2174P18.TR
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: M13-21;
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mdadams@tigr.org
Clones are available from Research
High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 476)
Mahairas, G.G., Wallace, J.C.,
                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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HS_4832_A1_E01_SP6E CIT Approved Human sapiens genomic clone Plate=4832 Col=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                              Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                   10449764
                                                                                                                                                                                                                                                                                                    Keller, A., Shaker, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ829617.1 GI:5795679
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.9%; Score 16; DB ilarity 100.0%; Pred. No. 1. Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA
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                                                                                                                                                                                                                                                                                                    Furlong, J., Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8;
J. 1.1e+02;
O;
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Row=I, genomic
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g,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 432;
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AV904180/c LOCUS DEFINITION

AV904180 AV904180

572 bp mRNA linear EST 09-NOV: Nori Satoh unpublished cDNA library, young adult Ciona

EST 09-NOV-2001

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AV903514/c
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Class: BAC ends
High quality sequence stop: 4
Location/Qualifiers
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Ciona intestinalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
                                                                                                                                                                                                                                                                                                                                                            Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
                                                                                                                                                                                                                                                                                                                                                                                         Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                    Email: satoh@ascidian.zool.kyoto-u.ac.jp.
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                                                                   ACCAAGCTTTTATAAT 16
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81-75-705-1113
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                                                                                              88.9%; Score 16; DB llarity 100.0%; Pred. No. 1. Conservative 0; Mismatches
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                                                                                                                                                                    /tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DN
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                           /organism="Ciona intestinalis"
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                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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AV904180
AV904180.1 GI:16893278
EST.
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Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
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1 (bases 1 to 618)
Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
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Location/Qualifiers
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                     Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                  Ciona intestinalis
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Department of Zoology
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Phlebobranchia; Cionidae; Ciona.
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adult"
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Search completed: February 10, 2005, 17:02:02 Job time : 124.68 secs

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Perfect score:
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Maximum DB seq length: 200000000
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Gapop_60.0 , Gapext 60.0
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1: /cgn2_6/ptodata/1/pubpna
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/ (cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq: *
/ (cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq: *
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/ (cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq: *
/ (cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq: *
/ (cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq: *
/ (cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq: *
/ (cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq: *
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	a		იი	!	Result
110	987	ი თ	ωu	22	٠ <del>۲</del>
68	70 68	101 70	118 118	498	Score
13.7 13.7	14.1 13.7 13.7	20.3	23.7 23.7	100.0	Query Match
	1501 1259 2480			i	Query Match Length DB
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US-09-991-209-36 US-09-991-209-25	4 US-10-012-013-44 0 US-09-991-209-43 9 US-10-678-588A-1	US-10-213-791-27 US-10-012-070A-49	US-09-872-051-8 US-10-790-430-8	US-09-872-051-7 US-10-790-430-7	ID
Sequence 36, Appl Sequence 25, Appl	Sequence 44, Appl Sequence 43, Appl Sequence 1, Appli	Sequence 27, Appl Sequence 49, Appl	Sequence 8, Appli Sequence 8, Appli	Sequence 7, Appli Sequence 7, Appli	Description

### ALIGNMENTS

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APPLICANT: Monsanto Co
APPLICANT: Behr, Carl
APPLICANT: Hironaka, Ca
APPLICANT: Heck, Gregoo
APPLICANT: You, Jinson
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Best Local Similarity 100
Matches 498; Conservative
                                                                                                                    SEQ ID NO 7
                                                                                                                                                                              APPLICANT: Heck, Gregory
APPLICANT: YOU, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Deted
TITLE OF INVENTION: Thereof
FILE REPERENCE: 38-21(52258)B
CURRENT APPLICATION NUMBER: US/10/790,430
CURRENT FILING DATE: 2004-03-01
PRIOR APPLICATION NUMBER: US/9/872,051
PRIOR APPLICATION NUMBER: US/9/872,051
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR FILING DATE: 2000-10-13
PRIOR PILING DATE: 2000-10-13
PRIOR PILING DATE: 2000-10-13
PRIOR FILING DATE: 2000-10-13
                                                                                                                                          NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version
                                        TYPE: DNA ORGANISM: Artificial
                                                                                             LENGTH: 498
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100.0%; Pred. No. 8.9e-262;
tive 0; Mismatches 0;
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                                                                                   APPLICANT: Behr, Carl
APPLICANT: Behr, Carl
APPLICANT: Hiromaka, Catherine
APPLICANT: Hiromaka, Catherine
APPLICANT: Hiromaka, Catherine
APPLICANT: Hiromaka, Catherine
APPLICANT: You, Jinsong
TITILE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for
TITILE OF INVENTION: Thereof
FILS REFERENCE: 38-21(52258)B
CURRENT APPLICATION NUMBER: US/09/872,051
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR FILING DATE: 2000-10-13
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09872051 Patent No. US20020013960A1
                    SOFTWARE: PatentIn
SEQ ID NO 8
LENGTH: 1183
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OTHER INFORMATION: 1-304 Zea maize genomic DNA
OTHER INFORMATION: 305-349 construct vector DNA
OTHER INFORMATION: 350-498 rice actin 1 promoter
TYPE: DNA
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Best Local Similarity
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Best Local Similarity
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APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Detec
TITLE OF INVENTION: Thereof
FILE REFERENCE: 38-21(52258)B
CURRENT APPLICATION NUMBER: US/10/790,430
CURRENT FILING DATE: 2004-03-01
PRIOR APPLICATION NUMBER: US/99/872,051
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-01-13
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SOFTWARE: PatentIn version 3.0
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APPLICANT: Behr, Carl
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OTHER INFORMATION: 1-164 Agrobacterium tumefaciens nos 3' terminator OTHER INFORMATION: 165-381 construct vector DNA
OTHER INFORMATION: 382-686 Zea maize plastid genes, rps11 and rpoA
OTHER INFORMATION: 687-1183 Zea maize genomic DNA
                                                                                                                                                                                                                                                                               NAME/KEY: source
LOCATION: (1):.(1183)
LOCATION: (1):.(1183)
OTHER INFORMATION: 1-164 Agrobacterium tumefaciens nos 3' terminator
OTHER INFORMATION: 165-381 construct vector DNA
OTHER INFORMATION: 382-686 Zea maize plastid genes, rps11 and rpoA
OTHER INFORMATION: 687-1183 Zea maize genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                       CGCGTGGTACCAAGCTTGATATCCCTAGGGCGGCCGCGTTAACAAGCTTACTCGAGGTCA 322
                                                                                                                                       CGCGTGGTACCAAGCTTGATATCCCCTAGGGCGGCCGCGTTAACAAGCTTACTCGAGGTCA 367
  TTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAAACAAAGGTAAGATTACC 264
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                                                                                                                                                                                                         Score 118; DB 18; Pred. No. 9.6e-54;
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Pred. No. 9.6e-54;
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; LOCATION: (2114)..(2369)
US-10-213-791-27
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TYPE: DNA
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Best Local S
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PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/108,763
PRIOR FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 32
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CURRENT FILING DATE: 2002-08-07
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                                                        APPLICANT: Pickerill, Andrew TITLE OF INVENTION: Herbicide Resistant Plants FILE REFERENCE: 50490/UST CURRENT APPLICATION NUMBER: US/10/012,070A CURRENT FILING DATE: 2001-10-29
                                                                                                                                                                        APPLICANT: Hawkes, Timothy APPLICANT: Warner, Simon APPLICANT: Andrews, Chris
PRIOR APPLICATION NUMBER: PCT/GB00/01573
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 57
                                                                                                                                                      APPLICANT:
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Local Similarity 100.0%; Pred. No. 2e-44;
res 101; Conservative 0; Mismatches
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Andrews, Christopher
Bachoo, Satvinder
Pickerill, Andrew
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to. US20030106096A1
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; ORGANISM: Oryza sp.
US-10-012-013-44
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US-10-012-013-44
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SEQ ID NO 44
LENGTH: 1501
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Publication No. US20030024009A1
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Best Local Similarity
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Publication No. US20030079246A1
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APPLICANT: Dunn-Coleman, Nigel
APPLICANT: Langdon, Timothy
APPLICANT: Langdon, Timothy
APPLICANT: Morse, Phillip
TITLE OF INVENTION: Manipulation of the Phenolic Acid
TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by
TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading
FILE REFERENCE: GC648-2
CURRENT APPLICATION NUMBER: US/09/991,209
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 60/249,608
PRIOR FILING DATE: 2000-11-17
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APPLICANT: Bachoo, Satvinder
APPLICANT: Pickerill, Andrew
TITLE OF INVENTION: Herbicide Resistant Plants
FILE REFERENCE: 50450/UST
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PRIOR FILING DATE: 2000-04-20
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ORGANISM: Oryza sp
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100.0%; Pred. No.
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Best Local S
Matches 68
                                                                                                                          Sequence 36, App
Publication No.
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LENGTH: 1259
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                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.2 SEQ ID NO 1
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                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Water-Deficit-TolerantTransgenic Plants
FILE REFERENCE: 38-21(52578)C
CURRENT APPLICATION NUMBER: US/10/678,588A
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,758
PRIOR PILING DATE: 2002-10-02
PRIOR PILING DATE: 2002-11-08
PRIOR PILING DATE: 2002-11-08
PRIOR PILING DATE: 2003-04-11
PRIOR PILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Langdon, Timothy
APPLICANT: Morse, Phillip
TITLE OF INVENTION: Manipulation of the Phenolic Acid
TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
                                                                                APPLICANT: Dunn-Coleman, Nigel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wu, Jingrui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: transcriptional unit comprising promoter, coding sequence for OTHER INFORMATION: transcription factor of SEQ ID NO:2 and terminator elements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: actin promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2480
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                                                                                                                        Application US/09991209
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                                                                                                                                                                                                                                                                                                                                                                                                     13.7%; Score 68; DB 19; 100.0%; Pred. No. 2.3e-26; tive 0; Mismatches 0;
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Sequence 25, Application US/09991209

Publication No. US20030024009A1

; BENERAL INFORMATION:

APPLICANT: Dunn-Coleman, Nigel
APPLICANT: Langdon, Timothy
APPLICANT: Morse, Phillip

TITLE OF INVENTION: Manipulation of the Phenolic Acid
TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes

FILE REFERENCE: GC648-2

CURRENT APPLICATION NUMBER: US/09/991,209

CURRENT FILING DATE: 2002-07-02

PRIOR APPLICATION NUMBER: US 60/249,608

PRIOR APPLICATION NUMBER: US 60/249,608

PRIOR APPLICATION SECOND-11-17

NUMBER OF SEQ ID NOS: 97

SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 60/249,608
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 5164
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RESULT 12
US-09-991-209-38
; Sequence 38, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: pTP5-1 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100 les 68; Conservative
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                                                                                                                                                                                                                              4050 CTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGGTA 4109
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100.0%; Pr
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PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 5295
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Langdon, Timothy
APPLICANT: Morse, Phillip
TITLE OF INVENTION: Manipulation of the Phenolic Acid
TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
FILE REFERENCE: GC648-2
CURRENT APPLICATION NUMBER: US/09/991,209
CURRENT APPLICATION NUMBER: US/09/991,209
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 60/249,608
PRIOR APPLICATION STORE OF SEQ ID NOS: 97
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FASTSEQ for Windows Version 4.0
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Publication No. US20030024009A1
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/991,209
CURRENT FILING DATE: 2002-07-02
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TITLE OF INVENTION: Manipulation of the Phenolic Acid
TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
                                                                                                                                                                                                            Query Match
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                          LENGTH: 5327
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                3876 CTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGGTA
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3936 AGATTACC 3943
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Morse, Phillip
                                        AGATTACC 425
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                                                                                                                                                                  13.7%; Score 68; DB 10; I larity 100.0%; Pred. No. 2.3e-26; Conservative 0; Mismatches 0;
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; OTHER INFORMATION: pTP8-5 vector
US-09-991-209-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: pTU4 vector US-09-991-209-19
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dunn-Coleman, Nigel
APPLICANT: Langdon, Timothy
APPLICANT: Langdon, Timothy
APPLICANT: Morse, Phillip
TITLE OF INVENTION: Manipulation of the Phenolic Acid
TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
TITLE REFERENCE: GC648-2
TURTENT APPLICATION NUMBER: US/09/991,209
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION UNMBER: US 60/249,608
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 5337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dunn-Coleman, Nigel
APPLICANT: Langdon, Timothy
APPLICANT: Mangdon, Timothy
APPLICANT: Morse, Phillip
TITLE OF INVENTION: Manipulation of the Phenolic Acid
TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
FILE REFERENCE: GC648-2
FILE REFERENCE: GC648-2
CURRENT APPLICATION NUMBER: US/09/991,209
CURRENT APPLICATION NUMBER: 050/2-07-02
PRIOR APPLICATION NUMBER: US 60/249,608
PRIOR PRILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 97
SOUTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: S337
                                                                                                            Matches
                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.7%; Score 68; DB 10; Length 5337; Best Local Similarity 100.0%; Pred. No. 2.3e-26; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4170 AGATTACC 4177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4110 CTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAAGGTA 4169
4110 CTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGGTA 4169
                               358 CTCGAGGTCATTCATATGCTTGAGAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGGTA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 CTCGAGGTCATTCATATGCTTGAGAAAGAGAGTCGGGATAGTCCAAAATAAAACAAAGGTA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         418 AGATTACC 425
                                                                                                      13.7%; Score 68; DB 10; ilarity 100.0%; Pred. No. 2.3e-26; Conservative 0; Mismatches 0;
                                                                                                                                                            Length 5337;
                                                                                                         Indels
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Qy 418 AGATTACC 425
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Db 4170 AGATTACC 4177
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Search completed: February 9, 2005, 11:12:26 Job time: 829.202 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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77.8 77.8 77.8 77.8		77.8 77.8 77.8		100.0 100.0 88.9 88.9	Query Match
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US-09-973-016-20184 US-09-671-317-418 US-09-891-641-34 US-08-421-661-5 US-09-949-016-4496	-09-949-016- -09-949-016- -09-949-016-	-09-949-016- -09-949-016- -09-949-016- -09-949-016- -09-949-016-	-09-422-978 -09-949-016 -09-949-016 -09-949-016 -09-949-016 -09-198-452 -09-016-434	US-09-872-051-11 US-09-872-051-8 US-09-949-016-81715 US-09-949-016-81717 US-09-949-016-14319 US-09-949-016-14120	ID
Sequence 403.04, App Sequence 34, Appl Sequence 5, Appli Sequence 5, Appli Sequence 4496, Ap			e 588 e 158 e 158 e 158 e 158 e 154	Sequence 11, Appl Sequence 8, Appli Sequence 81715, A Sequence 81717, A Sequence 14319, A Sequence 14120, A	Description

Sequence 8, Application US/09872051; Patent No. 6825400; GENERAL INFORMATION:

APPLICANT: Monsanto Co APPLICANT: Behr, Carl APPLICANT: Hironaka,

Hironaka, Catherine

RESULT 2 US-09-872-051-8

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Sequence 17	Sequence 11	Sequence 3,	Sequence 14.		Sequence 14				Sequence 16	Sequence 2,	Sequence 1,	٠,	۳	Sequence 1,	Sequence 1,	Ļ	
17474, A	11814, A	3, Appli	14394, A	14176, A	14580, A	14579, A	14177, A	16969, A	16968, A	Appli	riddy	Appli	Appli	TIGGA	TIGGA	TIGGA	Today,

### ALIGNMENTS

US-09-872-051-11

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                                                                                                                                                                           SOFTWARE: PatentIn version 3.0

SEQ ID NO 11

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
AAME/KEY: source
LOCATION: (1)..(18)
OTHER INFORMATION: Zea maize genomic DNA and vector
US-09-872-051-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09872051 Patent No. 6825400
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Best Local S
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                                                                                          Matches
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APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Det
TITLE OF INVENTION: Thereof
FILE REFERENCE: 38-21(52258)8
CURRENT APPLICATION NUMBER: US/09/872,051
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR PILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR PILING DATE: 2000-10-13
PRIOR PILING DATE: 2000-10-13
PRIOR PILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/240,014
PRIOR APPLICATION STEEL 2000-10-13
PRIOR FILING DATE: 2000-10-13
PRIOR PILING DATE: 2000-10-13
PRIOR PILING DATE: 2000-10-13
PRIOR PILING DATE: 2000-10-13
PRIOR PILING DATE: 2000-10-13
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                              1 TGCTGTTCTGCTGACTTT 18
                                                                                       l Similarity
18; Conserv
  TGCTGTTCTGCTGACTTT 18
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                                                                                       100.0%; ilarity 100.0%; Conservative 0;
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                                                                                                             Score 18; DB 4;
Pred. No. 0.54;
                                                                                            Mismatches
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Heck, Gregory

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                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-81715
                                                                                  Matches
                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                             SOFTWARE: FastSEQ
SEQ ID NO 81715
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS, IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 81715, Application US/09949016
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                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for DetecTITLE OF INVENTION: Thereof
FILE REFERENCE: 38-21(52258)B
CURRENT APPLICATION NUMBER: US/09/872,051
CURRENT FILING DATE: 2001-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-
NUMBER OF SEQ ID NOS: 16
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PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR FILING DATE: 2000-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: source
LOCATION: (1)..(1183)
COTHER INFORMATION: 1-164 Agrobacterium tumefaciens r
OTHER INFORMATION: 165-381 construct vector DNA
OTHER INFORMATION: 382-686 Zea maize plastid genes,
OTHER INFORMATION: 687-1183 Zea maize genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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  349
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TGCTGTTCTGCTGACT 334
                                         TGCTGTTCTGCTGACT 16
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                                                                                  Conservative
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                                                                                                   88.9%; Score 16;
100.0%; Pred. No.
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8;
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RESULT 4 US-09-949-016-81717/c

US-09-949-016-14120/c ; Sequence 14120, Application US/09949016

RESULT 6

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                                                                                                                                                ; FEATURE:

; MAME/KEY: misc feature

; LOCATION: (1)...(31391)

; OTHER INFORMATION: n = A,T,C or

US-09-949-016-14319
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; ORGANISM: Human
US-09-949-016-81717
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                                                                        Query Match
Best Local S
Matches 16
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Best Local
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                                                                                                                                                                                                                                                                                                   SEQ ID NO 14319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14319,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                LENGTH: 31
TYPE: DNA
                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION
                                                                                                                                                                                                                                              ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 601
 21183 TGCTGTTCTGCTGACT 21198
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                                     1 TECTETTCTECTEACT 16
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                                                                                             Similarity
                                                                          Conservative
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100.0%; Pr
0;
                                                                    88.9%; but
100.0%; Pr
                                                                                             Score 16; DB 4; ; Pred. No. 10;
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; LOCATION: (1)...(125192); OTHER INFORMATION: n = A,T,C US-09-949-016-14120
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION
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Patent No. 6537751
GENERAL INFORMATION:
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Best Local S
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LENGTH: 125192
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SEQ ID NO 7605
LENGTH: 21
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Best Local
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                                                                          Matches
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APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT SPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION STATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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EARLIER FILING DATE: 1998-04-21
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NAME/KEY: misc_feature
                                                                                                                                                               NAME/KEY: primer_bind
LOCATION: 1..21
OTHER INFORMATION: upstream amplification primer 99-9623 for SEQ 3671,
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ORGANISM: Homo Sapiens
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16; Conserva
                                                                      un 83.3%; Score 15; 1 Similarity 100.0%; Pred. No. 15; Conservative
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                                      CTGTTCTGCTGACTT 17
  CTGTTCTGCTGACTT 16
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Conservative 0;
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Pred. No.
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Query Match
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US-09-949-016-58184
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CURRENT FLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 000-09-08
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SEQ ID NO 58184
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                            Matches
                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                         TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(21125)
OTHER INFORMATION: n = A,T,C or
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11408
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  CTGTTCTGCTGACTT 11422
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100.0%; Pr
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US-09-949-016-13429/c

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; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5457
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                                                       Sequence 403, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 20
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
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SOFTWARE: FastSEQ for
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LOCATION: (1)...(57761)
OTHER INFORMATION: n = A,T,C
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APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
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                                                                                                                     NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 9793
LENGTH: 356
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Best Local (
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APPLICANT: Dumas Milne Edwards, J.B
                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                  TITLE OF INVENTION: ESTS and Encoded Human Proteins. FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (650) 845-41
INFORMATION FOR SEQ ID NO:
                                                                                                          TYPE: DNA
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LENGTH: 241 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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LIBRARY: BRUL
TWR: 2121175
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REGISTRATION NUMBER: 37
REFERENCE/DOCKET NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION:

APPLICANT: GATY Breton et. al

APPLICANT: GATY BRETON EN UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 4

LENGTH: 459

TYPE: DNA

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-4
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US-09-489-039A-4
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19121
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-19121
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US-09-949-016-19121/c
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Search completed: February 10, 2005, 08:50:03 Job time: 7.53136 secs
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT PILICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 77.8%; Score 14; DB 4; Length 459; Best Local Similarity 100.0%; Pred. No. 97; Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                        Query Match 77.8%; Score 14; DB 4; Best Local Similarity 100.0%; Pred. No. 98; Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19121, Application US/09949016 Patent No. 6812339
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/backfīles1.seq:*

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US-09-949-016-14813
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US-09-107-767-29026
US-09-270-767-13127
US-09-103-840A-1
US-09-103-840A-1
US-09-513-99C-15367
US-09-103-840A-1
US-09-104-1058-31
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                                     Sequence 10, Appli Sequence 14810, A Sequence 14811, A Sequence 14813, A Sequence 14813, A Sequence 14813, A Sequence 14813, A Sequence 13127, A Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 15367, A Sequence 15367, A Sequence 1685, Ap Sequence 21967, Ap Sequence 20395, A Sequence 20395, Sequence 20395, A Sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                            RESULT 2
US-09-872-051-8
    Sequence 8, Application US/09872051
Patent No. 6825400
GENERAL INFORMATION:
APPLICANT: Monsanto Co
APPLICANT: Behr, Carl
APPLICANT: Hironaka, Catherine
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28 12 66.7 813 3 US-09-056-556-3 29 12 66.7 813 4 US-09-072-967-3 30 12 66.7 813 4 US-09-072-967-3 31 12 66.7 1378 4 US-09-621-377B-1 32 12 66.7 1378 4 US-09-621-377B-1 33 12 66.7 1391 2 US-08-813-940-5 34 12 66.7 1414 4 US-09-270-767-11194 35 12 66.7 1497 4 US-09-270-767-11259 36 12 66.7 1688 2 US-09-270-767-11259 37 12 66.7 1688 2 US-09-716-865-13 38 12 66.7 1689 3 US-09-91-547A-1 38 12 66.7 2558 3 US-09-961-458C-1 39 12 66.7 3093 4 US-09-918-49 40 12 66.7 3093 4 US-09-614-221A-108 41 12 66.7 4175 3 US-08-306-6918-49 42 12 66.7 4175 5 PCT-US93-06251-84 45 12 66.7 9408 4 US-09-418-710-14 46 12 66.7 9408 4 US-09-418-710-14

### SOFTWARE: PatentIn version 3.0 SEQ ID NO 10 LENGTH: 18 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: NAME/KEY: SOURCE NAME/KEY: SOURCE LOCATION: (1)..(18) OTHER INFORMATION: zea maize pl US-09-872-051-10 밁 5 Matches Query Match APPLICANT: Heck, Gregory APPLICANT: You, Jinsong TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Det TITLE OF INVENTION: Thereof FILE REFERENCE: 38-21(52258)B CURRENT PELLCATION UNMEER: US/09/872,051 CURRENT FILING DATE: 2001-06-01 PRIOR APPLICATION NUMBER: 60/213,567 PRIOR APPLICATION NUMBER: 60/213,215 PRIOR PILING DATE: 2000-10-13 APPLICANT: 18; h 100.0%; Similarity 100.0%; Hironaka, Conservative Catherine maize plastid DNA 18 18 0; Score 18; DB 4; Pred. No. 0.036; Mismatches and vector 4. 0 Length 18; Indels DNA 0 Gaps 0,

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Best Local Similarity 100.0%; P
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                      SOFTWARE: Fast:
SEQ ID NO 14810
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CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 2000-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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PRIOR FILING DATE: 2000-10-13
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SOFTWARE: PatentIn version 3.0
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TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for DetecTITLE OF INVENTION: Thereof
FILE REFERENCE: 38-21(52258)B
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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LOCATION: (1)..(1183)
LOCATION: (1)..(1183)
OTHER INFORMATION: 1-164 Agrobacterium tumefaciens nos 3' terminator
OTHER INFORMATION: 165-381 construct vector DNA
OTHER INFORMATION: 382-686 Zea maize plastid genes, rps11 and rpoA
OTHER INFORMATION: 687-1183 Zea maize genomic DNA
                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)...(174170)
OTHER INFORMATION: n = A,T,C
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                                                                                                                                                                                                                                                       ORGANISM: Human
                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                           FastSEQ for Windows Version
CACGCGACACACTT 86920
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                                   CACGCGACACACTT 17
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                                                                           Mismatches
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ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(174318)
OTHER INFORMATION: n = A,T,C
US-09-949-016-11880
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                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/241,755 PRIOR FILING DATE: 2000-10-20
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CURRENT FILING DATE: 2000-04-14
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ORGANISM: Human
FEATURE:
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Local Similarity 100.0%; P.
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  Conservative
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77.8%; Score 14; DB 4; 100.0%; Pred. No. 9.5; tive 0; Mismatches
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Pred. No. 9.5;
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OF DETECTION AND USES THEREOF
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; LOCATION: (1)...(174318)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-14812
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION UNMEER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14812
                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14813
LENGTH: 174318
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Best Local
Query Match
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: CL001307
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                                                                NAME/KEY: misc_feature
LOCATION: (1)...(174318)
OTHER INFORMATION: n = A,T,C
                                                                                                                                       FEATURE:
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77.8%;
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  Score 14;
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OF DETECTION AND USES
Length 174318;
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US-09-313-294A-4452
RESULT 10
US-09-270-767-13127/c
03-09-270-767-13127/c
03-09-270-767-13127/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , NAME/KEY: misc_feature
, OTHER INFORMATION: Incyte ID No. 6476212 700348447H1
US-09-313-294A-4452
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; TYPE: DNA
; ORGANIZM: Drosophila melanogaster
US-09-270-767-29026
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US-09-270-767-29026/c
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SEQ ID NO 4452
LENGTH: 296
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Matches 14; Conserv
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29226
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APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLS OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION UMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: EPRL Program
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Best Local
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100.0%; Pr
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Pred. No.
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47;
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; Sequence 13127, Appl: ; Patent No. 6703491 ; GENERAL INFORMATION:

APPLICANT: Homburger et

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                                                                                                                      US-08-752-760A-1
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                                                         Query Match
Best Local S
Matches 13
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CURRENT APPLICATION NUMBER: US/09/270;767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13127
LENGTH: 1419
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GENERAL INFORMATION:
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Best Local 9
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                                                                                                                                                                                                                                       NAME: Seide, Rochelle K
REGISTRATION NUMBER: 32,300
REFERENCE/DOCKET NUMBER: A313
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-705-5000
TELEFAX: 212-705-5020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
                                                                                                                                                                                                            NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 35081 base pai
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/752,760A FILING DATE: 20-NOV-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                         Local Similarity
nes 13; Conserv
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STATE: NY
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
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STREET: 30 Rockefeller Plaza
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13; Conserv
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CGCGACACACTTC 6166
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                            CGCGACACACTTC 18
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                                                         72.2%; ilarity 100.0%; Conservative
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                                                                       Score 13;
Pred. No.
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                                                                                                                                                                                                                                          SEQ ID NO 1
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                                                                       Matches
                                                                                                       Query Match
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM FILE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                            APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRA:
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
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                                                                                                                                                         TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORWATION: H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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TYPE: DNA
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1224533 ACGCGACACACTT 1224521
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                                  5 ACGCGACACACTT 17
                                                                                        n 72.2%; Score 13; DB 3; Similarity 100.0%; Pred. No. 36;
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                                                                        Mismatches
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RESULT 14
US-09-513-999C-15367/c
; Sequence 15367, Application US/09513999C
; Patent No. 6783961

<u>,,</u>

Gaps

0

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NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent pm
SEQ ID NO 15367
LENGTH: 84
LENGTH: 84
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-15367
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US-09-513-999C-14094/c
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                                                  ; NAME/KEY: misc_feature
; LOCATION: 262
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-14094
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Best Local S
Matches 12
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APPLICANT: Giordano, J.Y.
TITLE OP INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-6
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 14094
LENGTH: 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14094, Application US/09513999C Patent No. 6783961
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 50
OTHER INFORMATION: n=a,
                                                                                                                                                                                                             LOCATION: 41
OTHER INFORMATION: n=a,
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LOCATION: 39
OTHER INFORMATION: s=g
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LOCATION: 35
OTHER INFORMATION: s=g or
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Matches 12; Conservative 0; Mismatches 0; Indels

Qy 2 ACCACGCGACAC 13

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Db 199 ACCACGCGACAC 188
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Search completed: February 10, 2005, 08:50:01 Job time : 18.5314 secs

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Title:
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Sequence:
                                                                                                                                                                                                                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                           Run on:
                                                                                                                                         Scoring table:
Minimum DB seq length: 0
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Gapop 60.0 , Gapext 60.0
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18
                                                                                              4708233 seqs, 24227607955 residues
                                                                                                                                                                  1 taccacgcgacacacttc 18
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                              9416466
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GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:* gb_om:
gb_pat:
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gb_rc:
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Database :

Post-processing: Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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•	14	14	14	15	15	15	15	15	15	15	15	15	15	15	16	17	18	18	Score
3	77.8	77.8	77.8	83.3	83.3	83.3	83.3	83.3	83.3	83.3	83.3	83.3	83.3	83.3	88.9	94.4	100.0	100.0	Query Match
727	435	435	435	349980	349115	325651	309400	299587	170777	110000	89474	69794	747	363	98319	865	1183	18	Query Match Length
ע	σ	σ	σ	σ	ب	۲	σ	N	N	N	N	N	0	11	W	9	σ	6	BB
00469539	AX308198	CQ508863	CQ499894	AX127152	BX927156	AP005283	AX127153	AC091307	AC148444	AP006502_01	AC013802	AC013773	AX065627	BV074353	AC090523	HSA325002	AX342369	AX342371	ID
00469529	AX308198	CQ508863	CQ499894	AX127152	BX927156	AP005283	AX127153	AC091307	AC148444	Continuation (2	AC013802	AC013773	AX065627	BV07435	AC090523	AJ325002	AX342369	AX342371	Description
Seguence	Sequence	Sequence	Sequence	Sequence	Corynebac	Corynebac	Sequence	Mus muscu	Rhinoloph	tion (2 of	Homo sapi	AC013773 Homo sapi	AX065627 Sequence	BV074353 S212P6009	Caenorhab	AJ325002 Homo sapi	Sequence	Sequence	ion

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AC007757 Drosophil	BX511107 Zebrafish	AC120554 Mus muscu	AC087768 Homo sapi	AP003492 Oryza sat	AC004586 Homo sapı	AC083928 Homo sapı	AF169823 Spodopter	AC142062 Rattus no		AC134824 Medicago	AY648026 Ovis arie	Continuation (11 o	Continuation (10 o	AC022280 Drosophil	AC017943 Drosophil	AC150979 Medicago	AC079522 Mus muscu	AC131498 Lytechinu	U40059 Caenorhabdi	AE007286 Sinornizo					

### ALIGNMENTS

RESULT 2 AX342369 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM	B &	Query Match Best Local : Matches 1:	source ORIGIN	JOURNAL FEATURES	ORGANISM REFERENCE AUTHORS TITLE	RESULT 1 AX342371 LOCUS DEFINITION ACCESSION VERSION VERSION VERSION VERVMORDS SOURCE
AX342369 1183 bp DNA linear PAT 12-JAN-2002 Sequence 8 from Patent EP1167531. AX342369 AX342369.1 GI:18151812 synthetic construct	1 TACCACGCGACACACTTC 18	ch 100.0%; Score 18; DB 6; Length 18; 1 Similarity 100.0%; Pred. No. 0.57; 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	118 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="zea maize plastid DNA and vector DNA"	Patent: EP 1167531-A 10 02-JAN-2002;  Monsanto Technology LLC (US)  Location/Qualifiers	synthetic construct other sequences. other sequences; artificial sequences.  Behr, C.F., Hironaka, C., Heck, G.R. and You, J. Corn transformant py-zmgt32 (nk603) and compositions and methods	AX342371 18 bp DNA linear PAT 12-JAN-2002 Sequence 10 from Patent EP1167531. AX342371 AX342371.1 GI:18151814 evnthetic construct

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REFERENCE
AUTHORS
TITLE
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AUTHORS
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1 (bases 1 to 865)

Kuteenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M., Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V., Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I., Kisselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R., Noti flanking sequences: a tool for gene discovery and verification of the human genome
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Submitted (16-MAY-2001) Microbiology
Karolinska Institute, Theorells vag,
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NL1-DK11R.
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Corn transformant pv-zmgt32 (nk603) and compositions and methods
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Zabarovsky, E.R.
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                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="NL1-DK11R"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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                                             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Murinae; Murinae; 1 (bases 1 to 363)
Wade,C.M., Kulbokas,E.J. III, Kirby,A.W., Zody,M.C., Mullikin,J.(Lander,E.S., Lindblad-Toh,K. and Daly,M.J.
The mosaic structure of variation in the laboratory mouse genome Nature 420 (6915), 574-578 (2002)
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BV074353
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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musculus STS genomic,

linear

STS 31-MAY-2003

Mullikin, J.C.,

Mus.

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98319 bp DNA linear INV 27-Caenorhabditis briggsae cosmid CB015N01, complete sequence.
AC090523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    summitted (27-FEB-2001) Department of Genetics, Washingto University, 4444 Forest Park Avenue, St. Louis, Missouri Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.
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Washington University Genome Sequencing Center.
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Department of Genetics, Washington University,
St. Louis, MO 63110, USA
                                                                                                                                                                                                                                                          /note="codon recognized: CUG" complement (67746. . . 67817)
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/clone="CB015N01"
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                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Caenorhabditis briggsae"
/mol_type="genomic DNA"
/strain="GujArat G16"
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                                                                                                                                                                                                           /product="tRNA-Pro"
/note="codon recognized: CCA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 CACGCGACACACTTC 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 6172580903
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/clone_lib="CZECHII/Ei"
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                                     /translation="mshtkpsiailgagrvgsslarsavaagyevkvagsgavdkial
Taeilmpgavpstadqavkdadivflavplhkfrsvnpatlegkividtmnhwvpvng
Eleeidqdprstseiiaeffagstmvksfnhigyheieqdagtgraiavatddvdaga
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                 QVAQLIKSFGFVPLNIGALENGRILEPGQEAFGAHLNKDSRLELVNQR"
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                                                                                                 codon_start=1/transl_table=11/protein_id="CAC26053.1"/db_xref="GI:12543340"
                                                                                                                                                                                                                             mol_type="unassigned
db_xref="taxon:1718"
                                                                                                                                                                                                                                                     organism="Corynebacterium glutamicum'
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-10A24
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HOMO Bapiens clone RP11-10A24, LOW-PASS SEQUENCE SAMPLING. AC013773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA On Jul 13, 2000 this sequence version replaced gi:6425747. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                               sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This record contains 77 individual
                                                                                                                                                                                                                                                                          be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
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9: gap of 100 bp 6: contig of 787 bp in le 6: gap of 100 bp	bp 16 bp in le bp 02 bp in le	5: gap of 1: 1: contig o	3: contig of 817 bp in le 3: gap of 100 bp	6: gap of 1	3: gap of 100 bp 4: contig of 821 bp in le	7: gap of 100 bp 3: contig of 826 bp in ler	4: gap of 100 bp 7: contig of 783 bp in le	5: gap of 100 bp 4: contig of 779 bp	1: contig of 821 bp in le 1: gap of 100 bp	0: contig of 813 bp in le	7: contig of 804 bp in le 7: gap of 100 bp	3: contig of 772 bp in le 3: gap of 100 bp	1: contig of 796 bp in le	5: contig of 823 bp i 5: gap of 100 bp	2: contig of 2: gap of 10	2: contig of 2: gap of 10	6: contig of 10	B: contig of B: gap of 10	8: contig of	3: contig of	6: contig of 10	4: contig of	7: contig of	3: contig of 813 bp in 1	0: contig of	2: contig of	6: contig of	9: contig of	3: contig of 10	5: contig of	5: contig of 5: gap of 10	5: contig of 10	8: gap of 10
OY 3 CCACGCGACACACTT 17	Query Match 83.3%; Score 15; DB 2; Length 69794; Best Local Similarity 100.0%; Pred. No. 26; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps	5 66185: contig of	7 64476: gap of 100 bp 7 65284: contig of 808 bp in 1	* 63484 63583: gap of 100 by in length  * 63584 64376: contig of 793 bp in length	1 62566: contig of 836 bp in le 7 62666: gap of 100 bp	9 61630: contig of 802 bp in 1 1 61730: gap of 100 bp	9 60728: contig of 760 bp in 1 9 60828: gap of 100 bp	7 59868: contig of 9 59968: gap of 100	58064: gap or 100 bp 5 58916: contig of 852 7 59016: gap of 100 bp	1 57180: gap or 100 1 57964: contig of	5 56264: gap of 100 5 57080: contig of	6 55385: gap of 100 bp 6 56164: contig of 779 bp in le	7 54456: gap of 100 bp 7 55285: contig of 829 bp in 1	4 53563: gap of 100 bp 4 54356: contig of 793 bp in le	<pre>52651: gap of 100 bp 53463: contig of 812 bp in len</pre>	9 51738: gap of 100 bp 9 52551: contig of 813 bp in ler	<pre>1 50840: gap of 100 bp 1 51638: contig of 798 bp in ler</pre>	7 49926: gap of 100 bp 7 50740: contig of 814 bp in ler	7 49056: gap of 100 bp 7 49826: contig of 770 bp in 1	0 48119: gap of 100 bp 0 48956: contig of 837 bp in 1	47223: gap of 100 bp 4 48019: contig of 796 bp	46319: GONCLY OF SEL DE THE A	45308: CONCLY OF 821 NO IN 1	44387; contig of 818 pp in 1 44487; gap of 100 bp in 1	43569: gap of 100 bp th te	9 42648: gap of 100 by	41710: gap of 100 bp	3 40822: gap of 100 bp 3 41610: contig of 788 bp in 1	9 39938: gap of 100 bp 9 40722: contig of 784 bp in 1	3 39017: gap of 100 bp 3 39838: contig of 821 bp in 1	38122: gap of 100 38917: contig of	37209: gap of 100 bp 38022: contig of 813	7 37109: contig of

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JOURNAL
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B birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., Maddonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassillev, H., VO, A., Wheeler, J., Wu, X.,
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-20M13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6957824. All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
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HTG; HTGS PHASE0.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                   the record is
be preserved.
                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L3932
Center clone name: 20_M_13
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Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B.,
Coleman, H., Daki, N., Engle, J., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B.,
Idol, J. R., Jones C., Karlins, B., Kim, H., Kwong, P., Laric, P.,
Larsulies, E. H., Masiello, C., Maskeri, B., McDowell, J.,
Margulies, E. H., Masiello, C., Maskeri, B., McDowell, J.,
Mullikin, J. C., Paguirigan, C., Portnoy, M. E., Prasad, A., Puri, O.,
Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C.,
Stantripop, S., Thomas, J. W., Thomas, P. J., Teipouri, V., Vogt, J.L.
Wetherby, K. D., Young, A. and Green, E. D.
MISC Comparative Sequencing Initiative
                                                                                     Submitted (01-APR-2004) NIH Intramural Sequencing Center, Grovemont Circle, Gatthersburg, MD 20877, USA On Apr 1, 2004 this sequence version replaced gi:44917669.
                                                                                                                                                                                        Submitted (04-MAR-2004) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 170777)
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Rhinolophus ferrumequinum (greater horseshoe bat)
Rhinolophus ferrumequinum
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                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                            Green, E.D.
                                                                                                                                                                                                                                                                                            Unpublished
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1 (bases 1 to 170777)
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Center: NIH Intramural Sequencing Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc zoo@nhgri.nih.gov
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 17243 tontig of 17243 bp in length

* 17244 17343: gap of unknown length

* 24933 25032: gap of unknown length

* 25033 75704: contig of 50672 bp in length

* 7505 75804: gap of unknown length

* 75805 95337: contig of 19533 bp in length

* 95338 95437: gap of unknown length

* 95338 95437: gap of unknown length

* 95338 95437: gap of unknown length

* 101417 101516: gap of unknown length

* 101417 101516: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces {\sf represented}
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101417
101517
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                                                                                                                                                                                                                                   vector_side:left"
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25033. .75704
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75805. .95337
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AC148387 clone VMRC7-122D13 (center project name gcl)"
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101517. .163768
                                                                                                                                                                                                                                                                                           note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           clone_lib="VMRC7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Rhinolophus ferrumequinum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
'note="assembly_fragment'
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                                                                                                                                                                                                                                                                                                                                                                                                .59786
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All Submitted (13-Apr.2001) Whitehead Institute/MIT Center for Genome R. 10 (1987)
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                                                                                                              Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y. Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Berreira, P., Fitzcerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., MacLea
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Macdonald.P., Major.J., Manning.J., Matthews,C., McCarthy,M.,
Meldarim,J., Meneus,L., Mihova,T., Mlenga,V., Murpby,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
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Mammalia; Butheria; Rodentia;
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/note="assembly_fragment clone_end:SP6
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100.0%; Pred. No. 24;
tive 0; Mismatches 0; Indels 0
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                                                                              Matthews, C., McCarthy, M.
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RESULT 12
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                                                                                                                                              4
                                                                                                                                                                                     l Similarity
15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 11, 2003 this sequence version replaced gi:24182398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rachupka, A.,
  AX127153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                      CACGCGACACACTTC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as soon as it is available and the accession number will be preserved.
                                                                                                       CACGCGACACACTTC 162247
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Contact: sequence submissions@genome.wi.mit.edu
----- Project Information
Center project name: L13257
Center clone name: 79_E_7
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261273
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                           clone_lib="RPCI-23 Female Mouse
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map="16"
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74183: gap of 100 bp
110439: contig of 36256 bp in length
110539: gap of 100 bp
135499: contig of 24960 bp in length
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contig of 18514
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gap of 100 bp
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of 55836 bp in length
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of 6558 bp in length
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KYOWA H
                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                   Submitted (24-MAY-2002) Satoshi Nakagawa, Kyowa Hakko Itd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Tokyo 194-8533, Japan (E-mail:snakagawa@xanagen.com,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum ATCC 13032
Corynebacterium glutamicum ATCC 13032
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7069 from Patent EP1108790. AX127153 AX114121
                                                                                                                                                                                                                                                                                                         Tel:81-44-829-3031,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakagawa, S.
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AP005283.1 GI:21
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                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete genomic sequence of Corynebacterium glutamicum ATCC 13032
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Ltd. And F
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|ence is conducted by collaboration
|And Kitasato University.
                                                                                                                  complement (135. .773)
/gene="Cg12799"
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/db_xref="taxon:1718"
/product="Molecular chaperone GrpE
/protein_id="BAC00193.1"
                                                                                              complement (135. .773)
                                                                                                                                                                                                                                                         Location/Qualifiers
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transl_table=11
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note="PF01025:GrpE"
                                                                                                                                                   'db_xref="taxon:196627"
'note="ATCC 13032"
                                                                                                                                                                                     mol_type="genomic DNA"
                                                                                                                                                                                                                        organism="Corynebacterium
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                 (heat shock protein)"
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/gene="Cgl28
3084. .4418
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SNGIDLTKDKNALQRLREABKAKIELSSSQSANINLFYITVDAKNFJEFLDETLSRA
EFQRITQBLLARTKTPERQVVKDAGVSVSEIDHVVLVGSTTRWFAVTELVKELTGGRE
EPQRITQBLLARTKTPERQVVKDGSVSSEIDHVLVLGSTTRWFAVTELVKELTGREF
PNKGVNPDEVVAVGAALQAGVLRGEVKDVLLLDVTFLSLGIETKGGVMTKLIERNTTI
PTKRSSTFTTALDNQFSVQIQVFQGEREIATANKLLGSSELGGIAPAPRGVPQIEVTF
DIDANGIVHTYAKDKGTGKENTITJDGSGLSQDEIDRMIKDAEAHADEBKKRREEDGI
DIDANGIVHTYAKDKGTGKENTTIDGOSGLSQDEIDRMIKDAEAHADEBKKRREEDGI
DIDANGIVHTYAKDKGTGKENTTIDGOSGLSQDEIDRMIKDAEAHADEBKKREEDGI
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VRNNAESLVYQTRKFVEENSEKVSEDLKAKVEEAAKGVEEALKGEDLEAIKA.VEKLN
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SdO

CDS

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complement (11995. .13032)

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Matches 15
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TITLE
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Corynebacterium glutamicum ATCC 13032

Corynebacterium glutamicum ATCC 13032

Corynebacterium glutamicum ATCC 13032

Corynebacterineae; Corynebacteriae; Actinobacteridae; Actinomycetales;

Corynebacterineae; Corynebacteriaceae; Corynebacterium.

1 (bases 1 to 349115)

Kalinowski,J., Bathe,B., Bartels,D., Bischoff,N., Bott,M.,
Burkovski,A., Dusch,N., Eggeling,L., Eixmanns,B.J., Gaigalat,L.,
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Rey,D.A., Ruckert,C., Rupp,O., Sahm,H., Wendisch,V.F., Wiegrabe,I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    349115 bp Corynebacterium glutamicum ATCC complete genome; segment 9/10.
BX927156 BX927147
BX977166
                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (21-JAN-2004) Joern Kalinowski, Institut fuer
Submitted (21-JAN-2004) Joern Kalinowski, Institut fuer
Genomforschung, Universitaet Bielefeld; Universitaetsstrasse
33615 Bielefeld, Germany
E-mail:Joern.Kalinowski@Cebitec.Uni-Bielefeld.DE
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J.
                                                                                                                                                                                      BX927157.1:51.
                                                                                                                                                                                                     BX927151.1:51. .349459, BX927152.1:51. .349799, BX927153.1:51. 
BX927154.1:51. .349575, BX927155.1:51. .349136, BX927156.1:51.
                                                                                                                                                                                                                                             BX927150.1:51. .348475,
                                                                                                                                                                                                                                                                  and Bielefeld University.
join(BX927148.1:1. .348071,BX927149.1:51.
                                                                                                                                                                                                                                                                                                           This sequence was accomplished by
                                                                                                                                                                                                                                                                                                                                                                                                                                      Kalinowski,J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 349115)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vitamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete Corynebacterium glutamicum ATCC 13032 genome sequence its impact on the production of L-aspartate-derived amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.3%; Score 15; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
                       /note="IS
307. .1917
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                                                                                                                                                . .349115
                                                                                                                                                                                      .140057)
                                        fingerprint type: 4-5"
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AAVLGS TAATANKA I SEVLMRVLDVIMS FPGIALAAVFWAYDGMGVPVI VFAIAFLY
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GCKS TTAMS INGLLPPTAKI EGGI LFDGKNLLDLKPDELNALRGHE IANI YQDALSSL
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TRNPRLI SAGMKQLTRRGGKRSAEELLELVGLDPKRTLGFAMI FYSHDLALVARLVHKLTV
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CDS

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gene
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AX127152/c
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Search completed: February 10, 2005, 13:13:51 Job time : 117.027 secs
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                                                                 328188 CACGCGACACACTTC
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Sequence 7068 from Patent EP1108790.
AX127152 AX114121
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                                                                                               4 CACGCGACACACTIC 18
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KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A. Novel polynucleotides
Patent: EP 1108790-A 7068 20-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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/locus_tag="cg2946"
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2.700.001 3.049.980"
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tive 0; Mismatches
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BI660197	CO879708	BI156664	CD342162	BU251290	CB457166	BY707912	BG764608	AJ452357	BX539441	BX905787	BI851715	CN274909	BI066464	CF571178	BQ038392	BG/12523	CB427482	#F578072	AU447864	CB066279
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## ALIGNMENTS

Query Match Best Local :	ORIGIN		source	FEATURES							COMMENT				JOURNAL					P	TITLE	AUTHORS			OKGANISM		SG		DEFINITION	756	RESULT 1		
Match 100.0%; Score 19; DB 9; Length 1489; Local Similarity 100.0%; Pred. No. 0.27;		/ sex="mate" /cell_type="lymphoblast" /clone_lib="PTB Chimpanzee Male BAC Library"	/Clone="PTB-115E10.R"	/mol_type="genomic DNA" /mb_type="genomic DNA" /mb_typef="traxon:9598"	/organism="Pan troglodytes"	Location/Qualifiers	R.Site 2 : SacI.	R.Site 1 : SacI	LIBRARY	Semiencing: Mi3Rev	clone tracking errors.	was generated during the R&D process and may have higher chance of	PTB This BAC	Tel:81-45-503-9111, Fax:81-45-503-9170)	<pre>L=/=22 SubmitO=CHOU, iButumit=ku, iOxOmama, immega=a 200 00:0, 002 (R=mail:chimphes@gsc.riken.go.jp/,</pre>	and Chemicar wesearch (kikky), Genomic Sciences Center (GSC), 1-7-22 Chemicar wesearch (Kikky), Genomic Sciences Center (GSC),	Submitted (02-AUG-2001) Asao rujiyama, The institute of ruysical	Direct Submission	Totoki, Y., Watanabe, H. and Sakaki, Y.	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,	2 (bases 1 to 1489)	Unpublished	BAC end sequences of Library PTB	rujiyama,A., Hattori,M., Toyoda,A., Tayior,1.v., Tada,1., Totoki.Y Watanabe,H. and Sakaki,Y.	1 Contract of Bosses and Bosses and Contract of the Contract o	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.	Rukarvota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;	Pan Crogrodyces (Chrimpanzee)		AG109756.1 GI:16730275	-115ElO.R, genomic survey	ACIONTEC 1489 hm DNA linear GSS 03-NOV-2001	

linear

EST 17-SEP-2003

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: poustka@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above EST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/ag_seaurchin/.cDNA
clones and filters are distributed via the Resource Center/Primary
Database of the German Human Genome Project (http://www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poustka,A.J., Groth,D., Hennig,S., Thamm,S., Cameron,A., Bec Reinhardt,R., Herwig,R., Panopoulou,G. and Lehrach,H. Generation, annotation, evolutionary analysis, and database integration of 20,000 unique sea urchin EST clusters Genome Res. 13 (12), 2736-2746 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Echinogylocentrotidae; Strongylocentrotus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTG 3' (M13RSP) 5'.seq BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP) 3'.seq Seq primer: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP) High quality sequence scop: 163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
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                                                                                                                                                          /clone lib="Sea urchin embryo 20hr blastula stage cDNA library MPMGP537"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1; Random primed and directionally cloned in pSport1 vector using a Not1 (5'-pGACTAGTTCTAGATCGCGAGCGGCCCC (T)15-3' and a Sal1 5'- TCGACCCACGCGTCCG-3'adapters (Gibco BRL)"
                                                                                                                                                                                                                                                                                                                                          /dev_stage="embryonic 20hr"
/lab_host="E.coli, XL1 blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                              clone="CALTp537E1217;MPI_537
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tive 0; Mismatches
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Fax: +49 30 8413 1128
Email: poustka@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above EST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/ag_seaurchin/. cDNA
clones and filters are distributed via the Resource Center/Primary
Database of the German Human Genome Project (http://www.rzpd.de)
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30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      StrPu537.002477 Sea urchin embryo 20hr blastula stage cDNA library MPMGp537 Strongylocentrotus purpuratus cDNA clone CALTp537K1047;MPI_537_47K10 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR PRIMERS
FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP) 5'-seq
BACKWARD: 5' CCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13RSP) 3'-sec
Seq primer: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13RSP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Max-Planck-Institut fuer Molekulare Genetik Ihnestr. 63-73, D-14195 Berlin, Germany
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CD324115.1 GI:34796176
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                                                                                                                                           Similarity
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                                                        TGTAGCGGCCCACGCGT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 333.
Location/Qualifiers
                                                                                                              Conservative
                                                                                                                                                                                                                                                       /note="Vector: pSportl; Site_1: Notl; Site_2: Sall; Random primed and directionally cloned in pSportl vector using a Notl [5'-pACTPACTICTMAATCGCGAGCGCCGCCC (T)15-3' and a Sall 5'- TCGACCCACGCGTCCG-3'adapters (Gibco BRL)"
                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Sea urchin embryo 20hr blastula stage cDNA
library MPMGp537"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:7668"
/clone="CALTp537K1047;MPI_537_47K10"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="embryonic 20hr"
/lab_host="E.coli, XL1 blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Strongylocentrotus purpuratus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="whole embryo'
                                                                                                                                         89.5%;
                                                                                                              0
                                                                                                                                         Score 17; DB 6;
Pred. No. 5.4;
                                                                                                                 Mismatches
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Length 333; Indels

Gaps

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RESULT 4
CD339324
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RESULT 5
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: poustka@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONP) to reduce sequencing redundancy. According to the ONF
(ONP) to reduce sequencing redundancy. According to the ONF
(ONP) to reduce sequencing redundancy. According to the ONF
(ONP) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above EST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/ag_seaurchin/.cDNA
clones and filters are distributed via the Resource Center/Primary
Database of the German Human Genome Project (http://www.rzpd.de)
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Contact: Poustka AJ Laboraty 145, dept.Lehrach
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD339324 461 bp mRNA linear StrPu536.003145 Sea urchin embryo 40hr gastrula st MPMGp536 Strongylocentrotus purpuratus cDNA clone CALTp536H0915;MPI_536_15H9 3', mRNA sequence. CD339324 CD339324.1 GI:34805850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
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                                                                                                                        TGTAGCGGCCCACGCGT 306
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Location/Qualifiers
                                                                                                                                                                                                                                       89.5%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                     /clone="CALTp536H0915;MPI_536_15H9"
/tissue_type="whole embryo"
/dev stage="embryonic 40hr"
/lab_host="E.coli, XLI blue"
/clone_lib="Sea urchin embryo 40hr gastrula stage cDNA
library MPMGp536"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1; Random
primed and directionally cloned in pSport1 vector using a
NotI [5'-pGACTAGTTCTAGATCGCGAGCGGCCCC (T)15-3' and a
Sal1 5'- TCGACCCACGCGTCCG-3'adapters (Gibco BRL)"
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/db_xref="taxon:7668"
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AUTHORS
TITLE
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AUTHORS
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BM607198/c
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              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoplante, a major partnership french program Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoplante.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Triticeae, Triticum.

1 (bases 1 to 570)
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                                                                                                                                                                      1 (bases 1 to 676)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L. Celera Anopheles gambiae EST project Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 33 1 69 47 54 00 Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoplante
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD912036.1 GI:32686360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
                                          Email: HoltRA@celera.com
Plate: NU01004AZS row: L
Seq primer: M13 Reverse.
                                                                                            Celera Genomics
45 w. Gude Dr., Rockville,
Tel: 2404533151
Fax: 2404534580
                                                                                                                                                                                                                                                                                                                                                                   676 bp 17000687084830 A.Gam.ad.cDNA.blood1 19600449683177 5', mRNA sequence 8M607198
                                                                                                                                                                                                                                                                                                   Anopheles gambiae
                                                                                                                                                         Contact: Holt R.A.
                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                   Anopheles gambiae (African malaria mosquito)
                                                                                                                                                                                                                                                                                                                                                  BM607198.1
                                                                                                                                                                                                                                                                       Neoptera; Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTAGCGGCCCACGCGT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="grain
pollination)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="G550"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cultivar="recital"
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/organism="Anopheles gambiae"
                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                      Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                                                                                                                                                                                                                                                                                                                                                    GI:18905302
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amali: Cgapbs remail.nin.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11137 row: h column: 09
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Location/Qualifiers
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/note="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and clones available through the Malaria Research and
                                                                                                                                                                                  /clone="IMAGE:5050424"
/lab_host="HH10B (T1 phage-resistant)"
/clone lib="NCI CGAP Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1
Site_2: Sall; Cloned unidirectionally. Primer: C
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="19600449683177"
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/lab_host="DH10b"
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                                                                                            89.5%; Score 17; DB 4; Length 752; 100.0%; Pred. No. 4.8;
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plate: LLAM14711 row: g column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 298)
                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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/lab host="PH10B (phage-resistant)"
/lab host="PH10B (phage-resistant)"
/clone lib="NICHD XGC_Kidl"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: Sal
/site 2: NotI; Cloned unidirectionally. Primer: Oligo c
Average insert size 2.2 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Cente
Clone distribution: NCI-GAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1961 Std Error: 0.00
Seq primer: -40UP from Gibco
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AQ464580

HS_5104_A1_G12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=680 Col=23 Row=M, genomic survey sequence. AQ464580

AQ464580.1 GI:4641675
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                             401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                              Sequence-tagged connectors: A sequence approach to mapping scanning the human genome proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 527)
Mahairas,G.G., Wallace,J.C.,
Keller,A., Shaker,R., Furlong
                                                                                                                                  High Throughput Sequencing Center University of Washington
                                                                                                                                                                               10449764
Contact: Mahairas GG, Wallace JC, Hood
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11.
library availability, please contact Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTAGCGGCCCACGCGT 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NCI_CGAP_Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Oligo dT.
Site_2: Noti; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
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/mol_type="mRNA"
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RESULT 11
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AUTHORS
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 680 row: M column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  546 bp DNA linear GSS 28-SEP-20 tigr-gss-dog-17000327426188 Dog Library Canis familiaris genomic, genomic survey sequence.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             Kirkness,E.F., Bafna,V., Halpern,A.L.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,
Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: T7
                                                                                                                                                                                                                       Contact: Kirkness BF
The Institute for Genomic Research
Department of Eukaryotic Genomics,
Rockville, MD 20850, USA
Tel: 301-338-0200
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canis familiaris
                                                                                                                                                                                   Email: ekirknes@tigr.org
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                     The dog genome: survey sequencing and comparative analysis science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
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                 /organism="Canis familiaris"
/mol type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone lib="Dog Library"
/note="Site 1: BstXI; Libraries w.
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Clone lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/male blood DNA was isolated from carndomly chosen do and partially dispested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/db_xref="taxon:9606"
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100.0%; Pr
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pred. No. 21;
mismatches
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21;
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Query Match Best Local Similarity

84.2%;

Score 16; Pred. No.

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Length 546;

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RESULT 12
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AUTHORS
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AUTHORS
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AG154721/c
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                               SSD
                                                                                                                                                                                 AG154721 651 bp DNA Pan troglodytes DNA, clone: RP43-018N05.T7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF983915.1 GI:12386727
EST.
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 Fujiyama, A., Hattori, M.,
                                                                         Pan troglodytes (chimpanzee)
Pan troglodytes
                                                                                                                              AG154721
AG154721.1
                                                                                                                                                                    sequence.
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Plate: LLAM10101 row: a column:
Plate: Licamitty sequence stop: 579.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                       Mammalia;
                                                        Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="duodenal adenocarcinoma, cell line"
/lab host="DHIOB (phage resistant)"
/clone libe"NIH_MCC_88"
/clone libe"NIH_MCC_88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: NotI, Site 2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                       Eutheria;
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                                   Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Pred. No.
 Toyoda, A.,
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 Taylor, T.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@sgc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library RPCI-43 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF983743 ...
602307337F1 NIH_MGC_88 Homo sapiens
                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                             1 (bases 1 to 1091)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
BF983743
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                            High quality sequence stop: 689
                                                                                                             Plate: LLAM10101 row: i column:
                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing: T7
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ite 1 : EcoRI
ite 2 : EcoRI.
Location/Qualifiers
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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100.0%; Pred. No. 20;
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CF842669
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Tyler,B. Not Published
Unpublished (2003)
Contact: Tyler B
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  62
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VBI
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5 GCGGCCCACGCGTGG 19
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Seq primer: BK reverse primer
High quality sequence stop: 251.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1880 Pratt Dr., Blacksburg, VA 24061, USA
Tel: 540-231-7318
Email: bmtyler@vt.edu
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CF842669.1 GI:38058323
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Phytophthora sojae
                                                                          h 78.9%; Score 15; DB 7; Length 251; Similarity 100.0%; Pred. No. 91; 15; Conservative 0; Mismatches 0; Indels
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/tissue_type="duodenal adenocarcinoma, cell line"
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/clone_lib="NIH MGC 88"
/clone_lib="NIH MGC 88"
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Site_1: NotI; Site_2: Sali; Cloned unidirectionally;
oligo-dT primed. Average insert size_1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
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/clone lib="USDA-IFAFS:Expression of Phytophthora sojae
genes during infection and propagation_sHB"
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| cgn2_6/ptodata/1/ina/5B_COMB.seq:*
| cgn2_6/ptodata/1/ina/6A_COMB.seq:*
| cgn2_6/ptodata/1/ina/6B_COMB.seq:*
| cgn2_6/ptodata/1/ina/6B_COMB.seq:*
| cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
| cgn2_6/ptodata/1/ina/backfIles1.seq:*
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US-09-902-540-970
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 RESULT 2
US-09-872-051-7
; Sequence 7, Application U
; Patent No. 6825400
; PATENTI INFORMATION:
; APPLICANT: MONGANTO CO
; APPLICANT: Hironaka, Ca
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Hironaka, Catherine

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                  Sequence 3, Application US/08390162 Patent No. 5576192 GENERAL INFORMATION:
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SEQ ID NO 9093
LENGTH: 843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: You, Jinsong
TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Detect TITLE OF INVENTION: Thereof
FILE REFERENCE: 38-21(52258)B
CURRENT APPLICATION NUMBER: US/09/872,051
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/213,567
PRIOR RILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/241,215
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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SOFTWARE: PatentIn version 3.0
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LOCATION: (1)..(498)
OTHER INFORMATION: 305-349 construct vector DNA
OTHER INFORMATION: 350-498 rice actin 1 promoter DNA
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Ichikawa, Atsushi
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100.0%; Pred. No. 0.092;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
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APPLICANT: Ichikawa, Atsushi
APPLICANT: Narumiya, Shuh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE: 24-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 064
PILING DATE: 23-MAR-1992
ATTORNEY/AGENT INFORMATION:
          ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ITITLE OF INVENTION: Production
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024179
FILING DATE: 23-FEB-1993
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                 TITLE OF INVENTION:
COMPUTER:
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CITY: Washington
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                                                                  COUNTRY: USA
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SOFTWARE: PatentIn Rela

OPERATING SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.25

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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
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NAME: FORDISTRATION NUMBER: 32,
        APPLICATION: 435
PILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION UMBER: US 08/024179
APPLICATION UMBER: US 08/024179
APPLICATION IMBER: 23.FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1405 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 24-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 00
FILING DATE: 23-MAR-1992
                                                                                                                            ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: JP 036580-1992
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APPLICATION NUMBER: US 08/024179
                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                631 TGTAGCGGCCCACGC 617
                                                                                                                                                                                                                                                                              Washington
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1300 I Street, N.W., Suite 700
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                                                                                                                                                                                                                                             USA
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24-FEB-1992
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               JP 036580-1992
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                                                               CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 036580-1992
FILING DATE: 24-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 064889-1992
FILING DATE: 23-WAR-1992
FILING DATE: 23-WAR-1992
ATTORNEY AGENT INFORMATION:
NAME: FORdis, Jean B.
REGISTRATION NUMBER: 32,984
REGISTRATION NUMBER: 04221-0020-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
 INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: JP 00
FILING DATE: 23-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,945B
FILING DATE: 22-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 08/024179
FILING DATE: 23-FEB-1993
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CORRESPONDENCE ADDRESS:
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                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
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nes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
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TELEPHONE: 202-408-4400
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1300 I Street, N.W., Suite
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ite 700
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11;
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SEQUENCE CHARACTERISTICS:

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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 6342
LENGTH: 2558
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                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
                                                                        CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 400
LENGTH: 2560
TYPE: DNA
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Patent No. 6833447
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Best Local Similarity
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ORGANISM: Myxococcus xanthus
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TOPOLOGY: lin
MOLECULE TYPE:
NAME/KEY: unsure
LOCATION: (1)..(2560)
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LOCATION: (1)..(2558)
OTHER INFORMATION: unsure at all n locations
                                                   ORGANISM: Myxococcus xanthus
                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.9%; Score 15; DB 4; 100.0%; Pred. No. 11;
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                                                                                                   ; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5440
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                                    Best Lo
                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 5440
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                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)8
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                 APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15949)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Goldman, Barry S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 10915
TYPE: DNA
ORGANISM: Myxococcus xanthus
                                                                                                                                                   ENGTH: 1083
                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 GTAGCGGCCCACGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 GTAGCGGCCCACGCG 166
                                    14;
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   3 TAGCGGCCCACGCG 16
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                                                    Similarity
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                                    Conservative
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                                 73.7%; Score 14; DB 4; 100.0%; Pred. No. 45; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.9%; Score 15; DB 4; 100.0%; Pred. No. 8.5;
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Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                   Length 1083;
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355 TAGCGGCCCACGCG 342

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Myxococcus xanthus US-09-902-540-8179
                                                                                                   RESULT 14
US-09-016-434-1361/c
                                                                                                                                                                                                                                                                                                                                                        US-09-826-509-556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 556, Application US/09826509 Patent No. 6806054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 8179
LENGTH: 1092
                                                          Sequence 1361, Application US/09016434 Patent No. 6500938
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Version 2.1
SEQ ID NO 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
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Best Local
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
EILE REFERENCE: 38-10(11549)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: US/09/902,540
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
RIOR APPLICATION OUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
RUMBER OF SEQ ID NOS: 16825
                                                                                                                                                                                                                                                                      Matches
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CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known
TITLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: AREN-207
                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1209
TYPE: DNA
ORGANISM: Homo sapiens
  APPLICANT:
                                                                                                                                                                                                                                                                      y Match 73.7%; Score 14;
Local Similarity 100.0%; Pred. No.
hes 14; Conservative 0; Mismatci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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                                                                                                                                                                                     536 TAGCGGCCCACGCG 523
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Janice Au-Young
Jeffrey J. Seilhamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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RESULT 15
US-08-068-729-3/c
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; CLONE: g410208
US-09-016-434-1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08068729 Patent No. 5985597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 31'.
CITY: PALO ALTO
CTATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: CONTITUE OF INVENTION: PA'S NUMBER OF SEQUENCES: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ford-Hutchinson, Anthony
APPLICANT: Funk, Colin
APPLICANT: Grygorczyk, Richard
APPLICANT: Metters, Kathleen
TITLE OF INVENTION: DNA Encoding Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                      COUNTRY: U
ZIP: 07065
                                                                                                                                                                                                                                        CITY: RAHWAY
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                ADDRESSEE: JULIA
ADDRES
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3174 PORTER DRIVE
                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Encoding Prostaglandin Receptor EP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1490
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   Version #1.25
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CURRENT APPLICATION NUMBER: US/08/068,729

FILING DATE: 26-MAY-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: WALLEN, JOHN W III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19012

TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEPHONE: (908) 594-3905
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

WOLECULE TYPE: cDNA
US-08-068-729-3

Query Match
Best Local Similarity 100.0%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 3 TAGCGGCCCACGCG 16
Db 610 TAGCGGCCCACGCG 597

Search completed: February 10, 2005, 08:49:48

Job time: 6.83865 secs
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11me : 6.83865 secs